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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 7751 Date: 5/24/06  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 872006300  
Location (Bldg/Room#): 2228 (Mailbox #): 2018 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Modn ab HIF 1 L  
Inventors (please provide full names): D T WARD et al.

Earliest Priority Date: 11/21/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID 20NA  
No: 446

Length limits betw 13 - 50 NTS  
12 - 50 NTS

70% Homology or greater  
SCORE OVER LENGTH SEARCH

No interference into bases

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Searcher: Jan

Searcher Phone #: 22504

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 6/6/06

Date Completed: 6/13/06

Searcher Prep & Review Time: 15

Online Time: 45

Type of Search

☒ NA Sequence (#)

☐ AA Sequence (#)

☐ Structure (#)

☐ Bibliographic

☐ Litigation

☐ Fulltext

☐ Other

Vendors and cost where applicable

☐ STN ☐ Dialog

☐ Questel/Orbit ☐ Lexis/Nexis

☐ Westlaw ☐ WWW/Internet

☒ In-house sequence systems

☒ Commercial ☐ Oligomer ☒ Score/Length  
☐ Interference ☐ SPDI ☐ Encode/Transl  
Other (specify) \_\_\_\_\_

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:51:49 ; Search time 0.001 Seconds  
(without alignments)  
12.960 Million cell updates/sec

Title: US-10-719-370A-446

Perfect score: 20  
Sequence: 1 cctcatggtcaccatgatga 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 324 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 12  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 25 summaries

Database : us-10-719-370a-446.sl.rml4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	19	1	US-08-846-020A-22
2	14.8	74.0	19	1	US-09-617-871-22
3	12.2	61.0	17	1	US-09-866-108A-7612
4	10.8	54.0	15	1	US-09-081-646-513
5	9.4	47.0	13	1	US-09-374-704-12
6	9.4	45.0	13	1	US-09-374-704-13
7	9.4	45.0	13	1	US-08-441-887A-200
8	8.4	42.0	12	1	US-08-030-335-10
9	8.4	42.0	12	1	US-07-973-431B-3
10	8.4	42.0	12	1	US-08-122-433-26
11	8.4	42.0	12	1	US-08-623-891-24
12	8.4	42.0	12	1	US-08-480-020B-10
13	8.4	42.0	12	1	US-08-910-618-10
14	8.4	42.0	12	1	US-09-105-515-2
15	8.4	42.0	12	1	US-08-910-322-10
16	8.4	42.0	12	1	US-08-679-493A-68
17	8.4	42.0	12	1	US-08-484-939A-10
18	8.4	42.0	12	1	US-09-340-861-24
19	8.4	42.0	12	1	US-09-634-262-24
20	8.4	42.0	12	1	US-09-748-044-2
21	8.4	42.0	12	1	US-09-384-472-10
22	8.4	42.0	12	1	US-09-835-370-54
23	8.4	42.0	12	1	US-09-793-146-38
24	8.4	42.0	12	1	US-09-793-146-48
25	8.4	42.0	12	1	US-09-793-146-49

## ALIGNMENTS

RESULT 1  
US-08-846-020A-22  
; Sequence 22, Application US/0846020A

Patent No. 6090547  
GENERAL INFORMATION:  
APPLICANT: Drazen M.D., Jeffrey M.  
APPLICANT: In M.D., Kwang-Ho  
APPLICANT: Asano M.D., Kolchiro  
APPLICANT: Beter, David  
APPLICANT: Grobholz, James  
TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence  
TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CHOATE, HALL & STEWART  
STREET: 53 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/846,020A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Jarell Ph.D., Brenda H.  
REGISTRATION NUMBER: 39,223  
REFERENCE/DOCKET NUMBER: 0092662-0012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-5000  
TELEFAX: (617) 248 4000  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
IMMEDIATE SOURCE:  
CLONE: Exon 4 sense primer  
US-08-846-020A-22  
Query Match 74.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 0.91;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CTCATGTCATGATG 19  
DB 2 CTCATGTCATGATG 19  
RESULT 2  
US-09-617-871-22  
; Sequence 22, Application US/09617871  
; Patent No. 6355434  
GENERAL INFORMATION:  
APPLICANT: Drazen M.D., Jeffrey M.  
APPLICANT: In M.D., Kwang-Ho  
APPLICANT: Asano M.D., Kolchiro  
APPLICANT: Beter, David  
APPLICANT: Grobholz, James  
TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence  
TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHOATE, HALL & STEWART  
STREET: 53 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA

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ZIP: 02109-2891
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/617,871
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,020
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0092662-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248 4000
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; IMMEDIATE SOURCE:
; CLONE: Exon 4 sense primer
US-09-617-871-22
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Query Match          74.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      2 CTCATGTCACATGATG 19
DB      2 CTCATGTCACATGATG 19
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RESULT 3
US-09-866-108A-7612/c
; Sequence 7612, Application US/09866108A
; Patent No. 6666188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7612
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7612
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Query Match          61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.8;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 CCTCATGTCACATGGA 17
DB      17 CCTCATGTCACATGGA 1
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RESULT 4
US-09-081-646-513
; Sequence 513, Application US/09081646
; Patent No. 633152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-513
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Query Match          54.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 4.4;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      4 CATGTCACATGGA 17
DB      1 CATGCCACAGTGA 14
```

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RESULT 5
US-09-374-704-12
; Sequence 12, Application US/09374704
; Patent No. 6958240
; GENERAL INFORMATION:
; APPLICANT: DERVAN, PETER B.
; APPLICANT: BAIRD, ELDON J.
; TITLE OF INVENTION: INHIBITION OF MAJOR GROOVE DNA BINDING
; FILE REFERENCE: 238/298
; CURRENT APPLICATION NUMBER: US/09/374,704
; CURRENT FILING DATE: 1999-08-12
; EARLIER APPLICATION NUMBER: PCT/US98/02664
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: PCT/US97/03332
; EARLIER FILING DATE: 1997-02-20
; EARLIER APPLICATION NUMBER: PCT/US97/12722
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; EARLIER FILING DATE: 1997-07-21
; EARLIER APPLICATION NUMBER: 60/038,384
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 60/023,309
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: 60/024,374
; EARLIER FILING DATE: 1996-08-01
; EARLIER APPLICATION NUMBER: 60/026,713
; EARLIER FILING DATE: 1996-09-25
; EARLIER APPLICATION NUMBER: 08/853,522
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: 08/837,524
; EARLIER FILING DATE: 1997-04-21
; EARLIER APPLICATION NUMBER: 08/607,078
; EARLIER FILING DATE: 1996-02-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Polyamide Motif
US-09-374-704-12

Query Match          47.0%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCATGTCACA 13
Db      3 TCATGTCACA 13

RESULT 6
US-09-374-704-13/c
; Sequence 13, Application US/09374704
; Patent No. 6958240
; GENERAL INFORMATION:
; APPLICANT: DERVAN, PETER B.
; APPLICANT: BAIRD, ELDON J.
; TITLE OF INVENTION: INHIBITION OF MAJOR GROOVE DNA BINDING
; TITLE OF INVENTION: PROTEINS BY MODIFIED POLYAMIDES
; FILE REFERENCE: 238/298
; CURRENT APPLICATION NUMBER: US/09/374,704
; CURRENT FILING DATE: 1999-08-12
; EARLIER APPLICATION NUMBER: PCT/US98/02684
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: PCT/US97/03332
; EARLIER FILING DATE: 1997-02-20
; EARLIER APPLICATION NUMBER: PCT/US97/12722
; EARLIER FILING DATE: 1997-07-21
; EARLIER APPLICATION NUMBER: 60/038,384
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 60/023,309
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: 60/024,374
; EARLIER FILING DATE: 1996-08-01
; EARLIER APPLICATION NUMBER: 60/026,713
; EARLIER FILING DATE: 1996-09-25
; EARLIER APPLICATION NUMBER: 08/853,522
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: 08/837,524
; EARLIER FILING DATE: 1997-04-21
; EARLIER APPLICATION NUMBER: 08/607,078
; EARLIER FILING DATE: 1996-02-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: GCM4 binding molecule
US-09-374-704-13

Query Match          47.0%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCATGTCACA 13
Db      11 TCATGTCACA 1

RESULT 7
US-08-441-887A-200/c
; Sequence 200, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipschutz, Robert J.
; APPLICANT: Lobban, Peter B.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2422
; TELEFAX: 650-326-2400
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-200

Query Match          45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CATGATGATA 20
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Db 11 |||||  
11 CATTGATGA 3

RESULT 8  
US-08-030-335-10/C  
Sequence 10, Application US/08030335

Patent No. 5491073  
GENERAL INFORMATION:  
APPLICANT: No. 5491073eborn, Mathews H  
APPLICANT: De Boer, Gerben F  
TITLE OF INVENTION: Cloning Of Chicken Anaemia DNA  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York, New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,335  
FILING DATE: 08-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Moran, Thomas F  
REGISTRATION NUMBER: 16,579  
REFERENCE/DOCKET NUMBER: 43276  
TELEPHONE: (212)-977-9550  
TELEFAX: (212)-977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-08-030-335-10

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGG 16  
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Db 12 GGTCACTGG 3

RESULT 9  
US-07-973-431B-3/C  
Sequence 3, Application US/07973431B

Patent No. 5652144  
GENERAL INFORMATION:  
APPLICANT: Lu, Yunchen  
APPLICANT: Haselcine, William A  
TITLE OF INVENTION: YC1 Protein, Gene, And Uses Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David G. Conlin; Dike, Bronstein,  
ADDRESSEE: Roberts & Cushman  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/973,431B  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30628  
REFERENCE/DOCKET NUMBER: 41968  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STR UR

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown

US-07-973-431B-3

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGG 16  
|||||  
Db 12 GGTCACTGG 3

RESULT 10  
US-08-122-433-26/C  
Sequence 26, Application US/08122433

Patent No. 5683985  
GENERAL INFORMATION:  
APPLICANT: Chu, Barbara C.F.  
APPLICANT: Ortel, Leslie  
TITLE OF INVENTION: OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH  
TITLE OF INVENTION: SELECTIVELY BIND TO DEFINED DNA SEQUENCES  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUGGEMANN & CLARK  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/122,433  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/687,337  
FILING DATE: 18-APR-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 9308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-1995  
TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-122-433-26

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16  
|||||  
DB 12 GGTCACGTGG 3

RESULT 11  
US-08-623-891-24/c  
Sequence 24, Application US/08623891  
Patent No. 5795778  
GENERAL INFORMATION:  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX  
NUMBER OF SEQUENCES: 115  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/623,891  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/238,200  
FILING DATE:  
APPLICATION NUMBER: US/07/987,133  
FILING DATE:  
APPLICATION NUMBER: 07/882,921  
FILING DATE: May 14, 1992  
APPLICATION NUMBER: 07/948,359  
FILING DATE: September 18, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Waiburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 200/209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-623-891-24

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGTCAC 12  
|||||  
DB 12 TCATGGCCAC 3

RESULT 12  
US-08-480-020B-10/c  
Sequence 10, Application US/08480020B  
Patent No. 5932476

GENERAL INFORMATION:  
APPLICANT: NOTEBORN, MATTHEUS H.M.  
TITLE OF INVENTION: CLONING OF CHICKEN ANEMIA DNA  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP  
STREET: 260 SHERIDAN AVENUE, SUITE 400  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,020B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/030,335  
FILING DATE: 08-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/NL91/00165  
FILING DATE: 12-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NL 9002008  
FILING DATE: 12-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: KUNG, VIOLA  
REGISTRATION NUMBER: P41,131  
REFERENCE/DOCKET NUMBER: VEOC.002.020US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)328-4400  
TELEFAX: (650)328-4477  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-020B-10

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16  
|||||  
DB 12 GGTCACGTGG 3

RESULT 13  
US-08-910-618-10/c  
Sequence 10, Application US/08910618  
Patent No. 5958424

GENERAL INFORMATION:  
APPLICANT: NOTEBORN, MATTHEUS H.M.  
TITLE OF INVENTION: CLONING OF CHICKEN ANEMIA DNA  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP  
STREET: 260 SHERIDAN AVENUE, SUITE 400

CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,618  
FILING DATE: 13-AUG-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,939  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/030,335  
FILING DATE: 08-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/NL91/00165  
FILING DATE: 12-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NL 9002008  
FILING DATE: 12-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: VEOC.002.01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)328-4400  
TELEFAX: (650)328-4477  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-910-618-10

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16  
DB 12 GGTCACGTGG 3

RESULT 14  
US-09-105-515-2/C  
Sequence 2, Application US/09105515  
Patent No. 6113913  
GENERAL INFORMATION:  
APPLICANT: BROUGH, DOUGLAS E.  
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900  
CITY: CHICAGO  
STATE: IL  
COUNTRY: US  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/105,515  
FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: KILYK JR., JOHN  
REGISTRATION NUMBER: 30763  
REFERENCE/DOCKET NUMBER: 83827  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5600  
TELEFAX: 312-616-5700  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-09-105-515-2

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16  
DB 12 GGTCACGTGG 3

RESULT 15  
US-08-910-322-10/C  
Sequence 10, Application US/08910322  
Patent No. 6238669  
GENERAL INFORMATION:  
APPLICANT: NOTEBOEN, MATHEUS H.M.  
TITLE OF INVENTION: CLONING OF CHICKEN ANEMIA DNA  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP  
STREET: 260 SHERIDAN AVENUE, SUITE 400  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,322  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,939  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/NL91/00165  
FILING DATE: 12-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NL 9002008  
FILING DATE: 12-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: VEOC.002.01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)328-4400  
TELEFAX: (650)328-4477  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-910-322-10

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGG 16  
DB 12 GGTCACTGG 3

RESULT 16

US-08-679-493A-68/C  
Sequence 68, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: TAYLOR, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 68  
LENGTH: 12  
TYPE: RNA  
ORGANISM: Human immunodeficiency virus type 1  
US-08-679-493A-68

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCATGCTCA 11  
DB 11 CTCATGCTCA 2

RESULT 17  
US-08-484-939A-10/C  
Sequence 10, Application US/08484939A  
Patent No. 6319693  
GENERAL INFORMATION:  
APPLICANT: NOTEBORN, MATHEUS H.M.  
TITLE OF INVENTION: CLONING OF CHICKEN ANEMIA DNA  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: RAE-VENTER LAW GROUP  
STREET: 260 SHERIDAN AVENUE, SUITE 400  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,939A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/030,335  
FILING DATE: 08-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/NL91/00165  
FILING DATE: 12-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: NL 9002008  
FILING DATE: 12-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: VEOC.002.01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)328-4400  
TELEFAX: (650)328-4477  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-939A-10

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGG 16  
DB 12 GGTCACTGG 3

RESULT 18  
US-09-340-861-24/C  
Sequence 24, Application US/09340861  
Patent No. 6432704  
GENERAL INFORMATION:  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HERPES SIMPLEX  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 115  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/340,861  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/987,133  
FILING DATE:  
APPLICATION NUMBER: 07/882,921  
FILING DATE: May 14, 1992  
APPLICATION NUMBER: 07/948,359  
FILING DATE: September 18, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 200/209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-340-861-24

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGCTCAC 12  
|||||  
DB 12 TCATGCTCAC 3

RESULT 19  
US-09-634-262-24/C  
Sequence 24, Application US/09634262  
Patent No. 6440719

GENERAL INFORMATION:  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX  
NUMBER OF SEQUENCES: 115  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/634,262  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/987,133  
FILING DATE:  
APPLICATION NUMBER: 07/882,921  
FILING DATE: May 14, 1992  
APPLICATION NUMBER: 07/948,359  
FILING DATE: September 18, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 200/209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-634-262-24

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGCTCAC 12  
|||||  
DB 12 TCATGCTCAC 3

RESULT 20  
US-09-748-044-2/C

Sequence 2, Application US/09748044  
Patent No. 6458578  
GENERAL INFORMATION:  
APPLICANT: Brough, Douglas E.  
APPLICANT: Kovsedl, Imre  
TITLE OF INVENTION: Recombinant Cell Line  
FILE REFERENCE: 207952  
CURRENT APPLICATION NUMBER: US/09/748,044  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: PCT/US99/14333  
PRIOR FILING DATE: 1999-06-24  
PRIOR APPLICATION NUMBER: US 09/105,515  
PRIOR FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Adenovirus type 5  
US-09-748-044-2

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16  
|||||  
DB 12 GGTCACATGG 3

RESULT 21  
US-09-384-472-10/C

Sequence 10, Application US/09384472  
Patent No. 6509446  
GENERAL INFORMATION:  
APPLICANT: NOTEBORN, MATHEUS H.M.  
APPLICANT: DE BOER, GERDEN F.  
TITLE OF INVENTION: CLONING OF CHICKEN ANEMIA DNA  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP  
STREET: 260 SHERIDAN AVENUE, SUITE 400  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/384,472  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,939  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/030,335  
FILING DATE: 08-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/NL91/00165  
FILING DATE: 12-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NL 9002008  
FILING DATE: 12-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: VEOC.002.01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 328-4400  
TELEFAX: (650) 328-4477

```

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 12 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-09-384-472-10

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Pred. No. 9.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCAATG 16
Db 12 GGTCACTG 3

RESULT 22
US-09-835-370-54
; Sequence 54, Application US/09835370
; Patent No. 6777544
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: base sequence of PNA derivatives that bind to
; OTHER INFORMATION: viral and cellular targets
US-09-835-370-54

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Pred. No. 9.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10
Db 2 CATCATGTC 11

RESULT 23
US-09-793-146-38
; Sequence 38, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-38

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Pred. No. 9.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10
Db 2 CATCATGTC 11

RESULT 24
US-09-793-146-48
; Sequence 48, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-48

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Pred. No. 9.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10
Db 2 CATCATGTC 11

RESULT 25
US-09-793-146-49/c
; Sequence 49, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
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US-09-793-146-49

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 9.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10  
Db 11 CATCATGTC 2

Search completed: June 13, 2006, 15:51:50  
Job time : 0.001 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:50:13 ; Search time 0.001 Seconds  
(without alignments)  
27.080 Million cell updates/sec

Title: US-10-719-370A-446

Perfect score: 20  
Sequence: 1 cctcatggtcaccatgatga 20

Scoring table: IDENTITY\_NTC  
Gapop 10.0 , Gapext 0.5

Searched: 37 seqs, 677 residues

Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 12  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 37 summaries

Database : us-10-719-370a-446.sl.rnpbms\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-10-719-370A-446	Sequence 446, App
2	19	95.0	20	US-10-719-370A-141	Sequence 141, App
3	19	95.0	20	US-10-719-370A-447	Sequence 447, App
4	18	90.0	20	US-10-719-370A-445	Sequence 445, App
5	18	90.0	20	US-10-719-370A-452	Sequence 452, App
6	17	85.0	20	US-10-766-185-26	Sequence 26, Appl
7	17	85.0	20	US-10-719-370A-451	Sequence 451, App
8	16	84.0	20	US-10-719-370A-443	Sequence 443, App
9	16	80.0	20	US-10-719-370A-448	Sequence 448, App
10	15	79.0	20	US-10-719-370A-450	Sequence 450, App
11	14	72.0	19	US-10-310-914A-757115	Sequence 757115,
12	14	72.0	19	US-11-083-784-440242	Sequence 440242,
13	14	72.0	19	US-11-101-244-440242	Sequence 440242,
14	13	69.0	19	US-11-083-784-15285	Sequence 15285, A
15	13	69.0	19	US-11-083-784-144519	Sequence 144519,
16	13	69.0	19	US-11-083-784-1218947	Sequence 1218947,
17	13	69.0	19	US-11-101-244-15285	Sequence 15285, A
18	13	69.0	19	US-11-101-244-144519	Sequence 144519,
19	13	69.0	19	US-11-101-244-1218947	Sequence 1218947,
20	13	67.0	19	US-11-083-784-155627	Sequence 155627,
21	13	67.0	19	US-11-083-784-155645	Sequence 155645,
22	13	67.0	19	US-11-083-784-943972	Sequence 943972,
23	13	67.0	19	US-11-083-784-1009396	Sequence 1009396,
24	13	67.0	19	US-11-083-784-1224506	Sequence 1224506,
25	13	67.0	19	US-11-101-244-155627	Sequence 155627,
26	13	67.0	19	US-11-101-244-155645	Sequence 155645,
27	13	67.0	19	US-11-101-244-943972	Sequence 943972,
28	13	67.0	19	US-11-101-244-1224506	Sequence 1224506,
29	13	67.0	19	US-11-101-244-1224506	Sequence 1224506,
30	12	61.0	17	US-09-866-108-7612	Sequence 7612, Ap
31	12	61.0	17	US-10-723-361-7612	Sequence 7612, Ap
32	11	57.0	15	US-09-916-466-30	Sequence 30, Appl
33	11	57.0	15	US-10-277-494-30	Sequence 30, Appl

## ALIGNMENTS

34	9.8	49.0	13	1	US-10-257-017B-228161	Sequence 228161,
C 35	9.8	49.0	13	1	US-10-257-017B-228162	Sequence 228162,
C 36	9.8	49.0	13	1	US-10-257-017B-245261	Sequence 245261,
C 37	9.8	49.0	13	1	US-10-257-017B-245262	Sequence 245262,
RESULT 1						
US-10-719-370A-446						
; Sequence 446, Application US/10719370A						
; Publication No. US20040220393A1						
; GENERAL INFORMATION:						
; APPLICANT: Ward, Donna T.						
; APPLICANT: Dobie, Kenneth W.						
; APPLICANT: Marcussen, Eric G.						
; APPLICANT: Freier, Susan M.						
; TITLE OF INVENTION: MODULATION OF HIF1A AND HIF2A EXPRESSION						
; FILE REFERENCE: ISPT-1010						
; CURRENT APPLICATION NUMBER: US/10/719,370A						
; CURRENT FILING DATE: 2003-11-21						
; PRIOR APPLICATION NUMBER: US 10/304,126						
; PRIOR FILING DATE: 2002-11-23						
; NUMBER OF SEQ ID NOS: 458						
; SOFTWARE: PatentIn version 3.2						
; SEQ ID NO 446						
; LENGTH: 20						
; TYPE: DNA						
; ORGANISM: Artificial Sequence						
; FEATURE:						
; OTHER INFORMATION: Synthetic Construct						
US-10-719-370A-446						
Query Match						
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;						
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	CCTCATGTCACATGATGA	20			
DB	1	CCTCATGTCACATGATGA	20			
RESULT 2						
US-10-719-370A-141						
; Sequence 141, Application US/10719370A						
; Publication No. US20040220393A1						
; GENERAL INFORMATION:						
; APPLICANT: Ward, Donna T.						
; APPLICANT: Dobie, Kenneth W.						
; APPLICANT: Marcussen, Eric G.						
; APPLICANT: Freier, Susan M.						
; TITLE OF INVENTION: MODULATION OF HIF1A AND HIF2A EXPRESSION						
; FILE REFERENCE: ISPT-1010						
; CURRENT APPLICATION NUMBER: US/10/719,370A						
; CURRENT FILING DATE: 2003-11-21						
; PRIOR APPLICATION NUMBER: US 10/304,126						
; PRIOR FILING DATE: 2002-11-23						
; NUMBER OF SEQ ID NOS: 458						
; SOFTWARE: PatentIn version 3.2						
; SEQ ID NO 141						
; LENGTH: 20						
; TYPE: DNA						
; ORGANISM: Artificial Sequence						
; FEATURE:						
; OTHER INFORMATION: Synthetic Construct						
US-10-719-370A-141						
Query Match						
Best Local Similarity 95.0%; Score 19; DB 1; Length 20;						
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	CCTCATGTCACATGATGA	19			

Db 2 CCTCATGTCACATGATGA 20

RESULT 3  
US-10-719-370A-447  
; Sequence 447, Application US/10719370A  
; Publication No. US20040220393A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Donna T.  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Marcuseon, Eric G.  
; APPLICANT: Freiler, Susan M.  
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION  
; FILE REFERENCE: ISPT-1010  
; CURRENT APPLICATION NUMBER: US/10/719,370A  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 10/304,126  
; PRIOR FILING DATE: 2002-11-23  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 447  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-719-370A-447

Query Match 95.0%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3 4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCATGTCACATGATGA 20  
Db 1 CTCATGTCACATGATGA 19

RESULT 4  
US-10-719-370A-445  
; Sequence 445, Application US/10719370A  
; Publication No. US20040220393A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Donna T.  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Marcuseon, Eric G.  
; APPLICANT: Freiler, Susan M.  
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION  
; FILE REFERENCE: ISPT-1010  
; CURRENT APPLICATION NUMBER: US/10/719,370A  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 10/304,126  
; PRIOR FILING DATE: 2002-11-23  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 445  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-719-370A-445

Query Match 90.0%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCATGGCAGATGATGA 20  
Db 1 TCATGGCAGATGATGA 18

RESULT 5

US-10-719-370A-452  
; Sequence 452, Application US/10719370A  
; Publication No. US20040220393A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Donna T.  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Marcuseon, Eric G.  
; APPLICANT: Freiler, Susan M.  
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION  
; FILE REFERENCE: ISPT-1010  
; CURRENT APPLICATION NUMBER: US/10/719,370A  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 10/304,126  
; PRIOR FILING DATE: 2002-11-23  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 452  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct

NAME/KEY: misc\_feature  
LOCATION: (11)..(11)  
NAME/KEY: misc\_feature  
LOCATION: (14)..(14)  
OTHER INFORMATION: n = inosine  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (14)..(14)  
OTHER INFORMATION: n = pseudouridine  
US-10-719-370A-452

Query Match 90.0%; Score 18; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 4.5;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATGATGA 20  
Db 1 CCTCATGTCACATGATGA 20

RESULT 6  
US-10-766-185-26  
; Sequence 26, Application US/10766185  
; Publication No. US20040152655A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoon, Heejeong  
; APPLICANT: Ahn, Chang Ho  
; APPLICANT: Lee, Young Bok  
; APPLICANT: Mao, Lingjun  
; APPLICANT: Jang, Xiaoming  
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1  
; FILE REFERENCE: REX 7034  
; CURRENT APPLICATION NUMBER: US/10/766,185  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: antisense oligonucleotide  
US-10-766-185-26

Query Match 85.0%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CATGTCACATGATGA 20  
Db 1 CATGTCACATGATGA 17

```
RESULT 7
US-10-719-370A-451
; Sequence 451, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Doble, Kenneth W.
; APPLICANT: Marcuseon, Eric G.
; APPLICANT: Freiler, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 451
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: n = Inosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n = pseudouridine
US-10-719-370A-451

Query Match      85.0%; Score 17; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 5.8;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 CCTCATGTCACATGATG 19
|||||
DB 2 CCTCATGTCACATGATG 20
|||||

RESULT 8
US-10-719-370A-443
; Sequence 443, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Doble, Kenneth W.
; APPLICANT: Marcuseon, Eric G.
; APPLICANT: Freiler, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 443
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-443
```

```
Query Match      84.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATGATG 20
```

```
DB 1 CCTCATGTCACATGATG 20
|||||

RESULT 9
US-10-719-370A-448
; Sequence 448, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Doble, Kenneth W.
; APPLICANT: Marcuseon, Eric G.
; APPLICANT: Freiler, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-448

Query Match      80.0%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CCTCATGTCACATG 16
|||||
DB 5 CCTCATGTCACATG 20
|||||

RESULT 10
US-10-719-370A-450
; Sequence 450, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Doble, Kenneth W.
; APPLICANT: Marcuseon, Eric G.
; APPLICANT: Freiler, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 450
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-450
```

```
Query Match      79.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.9;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATGATG 19
|||||
DB 2 CCTCATGTCACATGATG 20
|||||

RESULT 11
```

US-10-310-914A-757115/C  
; Sequence 757115, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kivazac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1389402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 757115  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-757115

Query Match 72.0%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 10;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGATGTCATCATGG 16  
| | | | | | | | | | | | | | | | | |  
DB 18 CCTGATGTCATCATGG 3

RESULT 12  
US-11-083-784-440242  
; Sequence 440242, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 440242  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-440242

Query Match 72.0%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATGTCATCATGATGA 20  
| | | | | | | | | | | | | | | | | |  
DB 4 AAGGUCACAGGAUGA 19

RESULT 13  
US-11-101-244-440242  
; Sequence 440242, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 440242  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-440242

Query Match 72.0%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATGTCATCATGATGA 20  
| | | | | | | | | | | | | | | | | |  
DB 4 AAGGUCACAGGAUGA 19

RESULT 14  
US-11-083-784-15285/C  
; Sequence 15285, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 15285  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-15285

Query Match 69.0%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCATGTCATGATGATG 19  
| | | | | | | | | | | | | | | | | |  
DB 18 TCATGTCATGATGATG 2

RESULT 15  
US-11-083-784-144519  
; Sequence 144519, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 144519
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-144519
```

```
Query Match          69.0%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 12;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 CCTCATGTCACATGGA 17
      |||:|||:|||:|||
Db      2 CAUCAGGUGACAUUGA 18
```

```

RESULT 16
US-11-083-784-1218947
; Sequence 1218947, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1218947
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1218947
```

```
Query Match          69.0%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 12;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 CCTCATGTCACATGGA 17
      |||:|||:|||:|||
Db      3 CCTCATGUGACAUUGA 19
```

```

RESULT 17
US-11-101-244-15285/c
; Sequence 15285, Application US/11101244
```

```

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 15285
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-15285
```

```
Query Match          69.0%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 TCATGGTCACATGATG 19
      |||:|||:|||:|||
Db      18 TCATGGTCACATGATG 2
```

```

RESULT 18
US-11-101-244-144519
; Sequence 144519, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 144519
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-144519
```

```
Query Match          69.0%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 12;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 CCTCATGTCACATGGA 17
      |||:|||:|||:|||
Db      2 CAUCAGGUGACAUUGA 18
```

```

RESULT 19
US-11-101-244-1218947
; Sequence 1218947, Application US/11101244
; Publication No. US20050246794A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1218947
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1218947

Query Match          69.0%; Score 13.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 12;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCTCATGTCATCATGGA 17
      |||:|:|:|:|:|:|
Db      3 CCUCAGUGGACAUUGA 19

RESULT 20
US-11-083-784-155627/c
; Sequence 155627, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 155627
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-155627

Query Match          67.0%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TGGTCACATGATGA 20
      |||||:|:|:|:|
Db      17 TGGTTACATGATGA 3

RESULT 21
US-11-083-784-155645/c
; Sequence 155645, Application US/11083784
```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 155645
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-155645

Query Match          67.0%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TGGTCACATGATGA 20
      |||||:|:|:|:|
Db      19 TGGTTACATGATGA 5

RESULT 22
US-11-083-784-943972
; Sequence 943972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 943972
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-943972

Query Match          67.0%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      6 TGGTCACATGATGA 20
      :|:|:|:|:|:|:|
Db      5 UGGUCCCAUGAUGA 19
```

RESULT 23  
US-11-083-784-1009396/c  
; Sequence 1009396, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1009396  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1009396

Query Match 67.0%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTCATG 15  
DB 15 CCTCAAGTCACATG 1

RESULT 24  
US-11-083-784-1224506  
; Sequence 1224506, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1224506  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1224506

Query Match 67.0%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TGTGCATGATGATGA 20  
DB 6 TGTGCATGATGATGA 20

Db 2 UGGUACAUCAUGA 16  
RESULT 25  
US-11-101-244-155627/c  
; Sequence 155627, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 155627  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-155627

Query Match 67.0%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TGTGCATGATGATGA 20  
DB 17 TGTTCATGATGATGA 3

RESULT 26  
US-11-101-244-155645/c  
; Sequence 155645, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 155645  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-155645

Query Match 67.0%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TGTGCATGATGATGA 20  
DB 19 TGTTCATGATGATGA 5



```

; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7612
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-7612

Query Match          61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCTCATGTCACATGGA 17
Db      17 CCTCAAGTCACAGGTA 1

RESULT 31
US-10-723-361-7612/c
; Sequence 7612, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7612
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-723-361-7612

Query Match          61.0%; Score 12.2; DB 1; Length 17;

; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7612
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-7612

Query Match          61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCTCATGTCACATGGA 17
Db      17 CCTCAAGTCACAGGTA 1

RESULT 32
US-09-916-466-30
; Sequence 30, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: MCSWIGEN, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Relat
; FILE REFERENCE: MBH00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-916-466-30

Query Match          57.0%; Score 11.4; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCATGTCACATG 15
Db      1 UCAGGUCACAAUG 13

RESULT 33
US-10-277-494-30
; Sequence 30, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSWIGEN, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-277-494-30

Query Match          57.0%; Score 11.4; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCATGTCACATG 15
Db      1 UCAGGUCACAAUG 13

RESULT 34
US-10-257-017B-228161
; Sequence 228161, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 228161
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055641
US-10-257-017B-228161

Query Match          49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 GTCACATGATGA 20
        |||||
Db      1 GTTACGTGATGA 13

RESULT 35
US-10-257-017B-228162/c
; Sequence 228162, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 228162
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055641
US-10-257-017B-228162

Query Match          49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 GTCACATGATGA 20
        |||||
Db      13 GTTACGTGATGA 1

RESULT 36
US-10-257-017B-245261
; Sequence 245261, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 245261
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059887
US-10-257-017B-245261

Query Match          49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 TGGTACATGAT 18
        |||||
Db      1 TGGTAACTGAT 13

RESULT 37
US-10-257-017B-245262/c
; Sequence 245262, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 245262
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059887
US-10-257-017B-245262

Query Match          49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 TGGTACATGAT 18
        |||||
Db      13 TGGTAACTGAT 1

Search completed: June 13, 2006, 15:50:13
Job time : 0.001 secs
```

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:46:01 ; Search time 0.001 Seconds  
(without alignments)  
46.240 Million cell updates/sec

Title: US-10-719-370a-446

Perfect score: 20

Sequence: 1 cctcatgctacatgatga 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 80 seqs, 1156 residues

Total number of hits satisfying chosen parameters: 160

Minimum DB seq length: 12

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 80 summaries

Database : us-10-719-370a-446.sl.rng4:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	ADT78875
2	19	95.0	20	1	ADT78876
3	19	95.0	20	1	ADT78571
4	18	90.0	20	1	ADT78881
5	18	90.0	20	1	ADT78874
6	17	85.0	20	1	ADQ88746
7	17	85.0	20	1	ADT78880
8	16	80.0	20	1	ADT78872
9	16	80.0	20	1	ADT78877
10	15	79.0	20	1	ADT78879
11	14	74.0	19	1	AAV13322
12	14	70.0	19	1	ADZ58131
13	14	70.0	19	1	ADZ57911
14	12	64.0	17	1	ABT38435
15	12	64.0	17	1	ADW14071
16	12	61.0	17	1	ABN07620
17	12	61.0	17	1	ACN12001
18	12	61.0	17	1	ACN70710
19	11	59.0	15	1	AAFS1883
20	11	59.0	15	1	AAFS1884
21	11	59.0	15	1	ADZ59539
22	11	57.0	15	1	ADZ59706
23	11	57.0	15	1	ADG13603
24	11	57.0	15	1	ADM69289
25	11	56.0	15	1	ADNR4253
26	11	55.0	15	1	ABK09404
27	11	55.0	15	1	ACLT3850
28	11	55.0	15	1	ACLT3880
29	11	55.0	15	1	ACLT3792
30	10	54.0	14	1	ADL96404
31	10	54.0	15	1	AAK1458
32	10	54.0	15	1	AAFS1885
33	10	54.0	15	1	AAFS1882

34	10.8	54.0	15	1	ABK32412	Human colon cancer
35	10.4	52.0	14	1	ADQ82962	Extended hairpin t
36	10.4	52.0	14	1	ADQ82964	Extended hairpin t
37	10	50.0	14	1	AAI36745	Antisense oligonuc
38	10	50.0	14	1	AAH89017	Human polymorphic
39	9.8	49.0	13	1	ABH45285	Oligonucleotide SE
40	9.8	49.0	13	1	ABH45284	Oligonucleotide SE
41	9.8	49.0	13	1	ABH28185	Oligonucleotide SE
42	9.8	49.0	13	1	ABH28184	Oligonucleotide SE
43	9.8	49.0	14	1	AAV70553	Sequence of probe
44	9.4	47.0	13	1	AAI19052	Human PPAR-gamma-3
45	9.4	47.0	13	1	ADZ24722	Human SNP detectio
46	9.4	47.0	13	1	ADP86939	Polyamide-binding
47	9.4	47.0	13	1	ADP86940	Polyamide-binding
48	9	45.0	12	1	AAQ88597	Human mitochondria
49	9	45.0	12	1	AAV32269	Random primed reve
50	8.8	44.0	12	1	AAH23540	Antibacterial pep
51	8.8	44.0	12	1	ABH82120	Oligonucleotide pr
52	8.8	44.0	12	1	ABH08296	Oligonucleotide pr
53	8.8	44.0	12	1	ADW11578	siRNA production-r
54	8.4	42.0	12	1	AAQ24034	Herpesvirus inhibi
55	8.4	42.0	12	1	AAQ30497	Adenovirus major 1
56	8.4	42.0	12	1	AAQ52946	Herpes simplex vir
57	8.4	42.0	12	1	AAZ59958	Adenovirus Ads maj
58	8.4	42.0	12	1	AAI30866	Fragment of a plas
59	8.4	42.0	12	1	ABH48155	Oligonucleotide pr
60	8.4	42.0	12	1	ABH35107	Oligonucleotide pr
61	8.4	42.0	12	1	ABH72389	Oligonucleotide pr
62	8.4	42.0	12	1	ABH84083	Oligonucleotide pr
63	8.4	42.0	12	1	ABH04761	Oligonucleotide pr
64	8.4	42.0	12	1	ABH67680	Oligonucleotide pr
65	8.4	42.0	12	1	ABH08303	Oligonucleotide pr
66	8.4	42.0	12	1	ABH29750	Oligonucleotide pr
67	8.4	42.0	12	1	AAH49257	PNA-forming oligon
68	8.4	42.0	12	1	AAH49256	PNA-forming oligon
69	8.4	42.0	12	1	AAH49260	PNA-forming oligon
70	8.4	42.0	12	1	AAH49261	PNA-forming oligon
71	8.4	42.0	12	1	AAH49259	PNA-forming oligon
72	8.4	42.0	12	1	AAH49258	PNA-forming oligon
73	8.4	42.0	12	1	ABH82718	Human protective D
74	8.4	42.0	12	1	ABK72560	Human OPA1 gene, e
75	8.4	42.0	12	1	ABH01332	HIV-1 rev oligonuc
76	8.4	42.0	12	1	ABH98610	Modified peptide n
77	8.4	42.0	12	1	ABH97503	Peptide nucleic ac
78	8.4	42.0	12	1	ADW56294	Mouse Slc26a6 anio
79	8.4	42.0	12	1	ADQ29965	Rat VRI exon 1d tr
80	8.4	42.0	12	1	AEF80873	MLTf/USF promoter

## ALIGNMENTS

RESULT 1	ADT78875	standard; DNA; 20 BP.
ID	ADT78875	
AC	ADT78875;	
DT	27-JAN-2005	(first entry)
XX	Antisense oligonucleotide (ISIS 330449) for human HIF1alpha.	
XX		
XX	Antisense therapy; human; hypoxia-inducible factor 1 alpha;	
KW	hypoxia-inducible factor 2 alpha; HIF1alpha; HIF1alpha;	
KW	hyperproliferative disorder; cancer; p53; angiogenic disorder;	
KW	eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;	
KW	psoriasis; atherosclerosis; smooth muscle cell proliferation;	
KW	blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;	
KW	ophthalmological; antiinflammatory; respiratory; vasotropic; ss.	
OS	Homo sapiens.	
XX		
PN	US2004220393-A1.	

```
XX 04-NOV-2004.
XX
XX 21-NOV-2003; 2003US-00719370.
XX
XX 23-NOV-2002; 2002US-00304126.
XX
XX (WARD/) WARD D T.
XX (DOBI/) DOBIE K W.
XX (MARC/) MARCUSSEN E G.
XX (FREI/) FREIER S M.
XX
XX Ward DT, Dobie KW, Marcussen EG, Freier SM;
XX WPI; 2004-774955/76.
XX
XX New antisense compound which inhibits the expression of hypoxia-inducible
XX factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
XX hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
XX Claim 92; SEQ ID NO 446; 195bp; English.
XX
XX The present invention relates to antisense compounds targeted to nucleic
XX acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
XX hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
XX comprises an antisense oligonucleotide that specifically hybridises with
XX the nucleic acid and inhibits the expression of HIF1alpha and/or
XX HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
XX The antisense oligonucleotide comprises at least one modified
XX internucleoside linkage, preferably a phosphorothioate linkage. It also
XX comprises at least one modified sugar moiety, preferably a 2'-O-
XX methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
XX comprises at least one modified nucleobase, preferably a 5-
XX methylcytosine. The antisense oligonucleotides are useful for the
XX treatment of diseases such as hyperproliferative disorders, e.g. cancer,
XX preferably a cancer carrying a p53 mutation, or an angiogenic disorder
XX that affects the eye. The compound is also useful for treating tumours,
XX hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
XX atherosclerosis and smooth muscle cell proliferation in the blood vessels
XX such as stenosis or restenosis following angioplasty. It is also useful
XX in drug discovery and target validation, and can be utilised for
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX The present sequence represents an oligonucleotide used in the examples
XX of the present invention.
XX
XX SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.7;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCTCATGTCACATGATGA 20
XX ||||||||||||||||
XX Db 1 CCTCATGTCACATGATGA 20
XX
XX RESULT 2
XX ADT78876
XX ID ADT78876 standard; DNA; 20 BP.
XX
XX AC ADT78876;
XX
XX DT 27-JAN-2005 (first entry)
XX
XX DE Antisense oligonucleotide (ISIS 330448) for human HIF1alpha.
XX
XX Antisense therapy; human; hypoxia-inducible factor 1 alpha;
XX hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
XX hyperproliferative disorder; cancer; p53; angiogenic disorder;
XX eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
XX psoriasis; atherosclerosis; smooth muscle cell proliferation;
XX blood vessel; restenosis; angioplasty; cyclostatic; angiogenesis;
XX ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
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```
XX Homo sapiens.
XX
XX US2004220393-A1.
XX
XX 04-NOV-2004.
XX
XX 21-NOV-2003; 2003US-00719370.
XX
XX 23-NOV-2002; 2002US-00304126.
XX
XX (WARD/) WARD D T.
XX (DOBI/) DOBIE K W.
XX (MARC/) MARCUSSEN E G.
XX (FREI/) FREIER S M.
XX
XX Ward DT, Dobie KW, Marcussen EG, Freier SM;
XX WPI; 2004-774955/76.
XX
XX New antisense compound which inhibits the expression of hypoxia-inducible
XX factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
XX hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
XX Claim 92; SEQ ID NO 447; 195bp; English.
XX
XX The present invention relates to antisense compounds targeted to nucleic
XX acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
XX hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
XX comprises an antisense oligonucleotide that specifically hybridises with
XX the nucleic acid and inhibits the expression of HIF1alpha and/or
XX HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
XX The antisense oligonucleotide comprises at least one modified
XX internucleoside linkage, preferably a phosphorothioate linkage. It also
XX comprises at least one modified sugar moiety, preferably a 2'-O-
XX methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
XX comprises at least one modified nucleobase, preferably a 5-
XX methylcytosine. The antisense oligonucleotides are useful for the
XX treatment of diseases such as hyperproliferative disorders, e.g. cancer,
XX preferably a cancer carrying a p53 mutation, or an angiogenic disorder
XX that affects the eye. The compound is also useful for treating tumours,
XX hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
XX atherosclerosis and smooth muscle cell proliferation in the blood vessels
XX such as stenosis or restenosis following angioplasty. It is also useful
XX in drug discovery and target validation, and can be utilised for
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX The present sequence represents an oligonucleotide used in the examples
XX of the present invention.
XX
XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 95.0%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.4;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 CTCATGTCACATGATGA 20
XX ||||||||||||||||
XX Db 1 CTCATGTCACATGATGA 19
XX
XX RESULT 3
XX ADT78571
XX ID ADT78571 standard; DNA; 20 BP.
XX
XX AC ADT78571;
XX
XX DT 27-JAN-2005 (first entry)
XX
XX DE HIF1alpha cDNA, antisense oligonucleotide ISIS #298697.
XX
XX Antisense therapy; human; hypoxia-inducible factor 1 alpha;
XX hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
XX hyperproliferative disorder; cancer; p53; angiogenic disorder;
```

KM eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;  
 KM psoriasis; atherosclerosis; smooth muscle cell proliferation;  
 KM blood vessel; restenosis; angioplasty; cyostatic; angiogenesis;  
 KM ophthalmological; antiinflammatory; respiratory; vasotropic; mouse; rat;  
 KM phosphorothioate; ss.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 OS Rattus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone. All cytidines are 5-methylcytidines"  
 FT 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"  
 FT 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"  
 XX  
 XX US2004220393-A1.  
 PD 04-NOV-2004.  
 XX  
 XX 21-NOV-2003; 2003US-00719370.  
 PF  
 XX 23-NOV-2002; 2002US-00304126.  
 PR  
 XX (WARD/) WARD D T.  
 PA (DOB/) DOBIE K W.  
 PA (MARC/) MARCUSON E G.  
 PA (FREI/) FREIER S M.  
 XX  
 XX Ward DT, Dobie KM, Marcusson EG, Freier SM,  
 PI WPI; 2004-774955/76.  
 DR  
 XX  
 XX New antisense compound which inhibits the expression of hypoxia-inducible factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating hyperproliferative disorder, e.g. cancer carrying a p53 mutation.  
 PT  
 PT  
 XX  
 XX Claim 27; SEQ ID NO 141; 195pp; English.  
 PS  
 XX  
 XX The present invention relates to antisense compounds targeted to nucleic acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound comprises an antisense oligonucleotide that specifically hybridizes with the nucleic acid and inhibits the expression of HIF1alpha and/or HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, preferably a phosphorothioate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5-methylcytosine. The antisense oligonucleotides are useful for the treatment of diseases such as hyperproliferative disorders, e.g. cancer, preferably a cancer carrying a p53 mutation, or an angiogenic disorder that affects the eye. The compound is also useful for treating tumours, hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis, atherosclerosis and smooth muscle cell proliferation in the blood vessels such as stenosis or restenosis following angioplasty. It is also useful in drug discovery and target validation, and can be utilized for CC diagnosis, therapeutics, prophylaxis and as research reagents and kits. CC The present sequence represents an antisense oligonucleotide used in the CC examples of the present invention.  
 CC  
 CC Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 XX

Query Match 95.0%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CCTCATGTCACATGATG 19  
 |||||  
 Db 2 CCTCATGTCACATGATG 20  
 RESULT 4  
 ADT78881  
 ID ADT78881 standard; DNA; 20 BP.  
 XX  
 AC ADT78881;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 XX Antisense oligonucleotide (ISIS 337224) for human HIF1alpha/HIF2alpha.  
 DE  
 XX  
 XX Antisense therapy; human; hypoxia-inducible factor 1 alpha;  
 KM hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;  
 KM hyperproliferative disorder; cancer; p53; angiogenic disorder;  
 KM eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;  
 KM psoriasis; atherosclerosis; smooth muscle cell proliferation;  
 KM blood vessel; restenosis; angioplasty; cyostatic; angiogenesis;  
 KM ophthalmological; antiinflammatory; respiratory; vasotropic; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 11  
 FT /\*tag= a  
 FT /mod\_base= 1  
 FT 14  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Pseudouridine"  
 XX  
 XX US2004220393-A1.  
 PN  
 XX  
 XX 04-NOV-2004.  
 PD  
 XX  
 XX 21-NOV-2003; 2003US-00719370.  
 PF  
 XX 23-NOV-2002; 2002US-00304126.  
 PR  
 XX (WARD/) WARD D T.  
 PA (DOB/) DOBIE K W.  
 PA (MARC/) MARCUSON E G.  
 PA (FREI/) FREIER S M.  
 XX  
 XX Ward DT, Dobie KM, Marcusson EG, Freier SM,  
 PI WPI; 2004-774955/76.  
 DR  
 XX  
 XX New antisense compound which inhibits the expression of hypoxia-inducible factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating hyperproliferative disorder, e.g. cancer carrying a p53 mutation.  
 PT  
 PT  
 XX  
 XX Example 30; SEQ ID NO 452; 195pp; English.  
 PS  
 XX  
 XX The present invention relates to antisense compounds targeted to nucleic acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound comprises an antisense oligonucleotide that specifically hybridizes with the nucleic acid and inhibits the expression of HIF1alpha and/or HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, preferably a phosphorothioate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5-methylcytosine. The antisense oligonucleotides are useful for the



CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'  
CC aatggcaccgcgtctccaa 3' and SEQ ID NO. 4, 5' ggagctaccctcccaatc 3',  
CC respectively). The compounds are useful for inhibiting the expression of  
CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
CC antisense compounds are also useful for preventing or delaying infection,  
CC inflammation, or tumor formation. This sequence represents a human HIF-1  
CC antisense oligonucleotide.  
XX  
SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 85.0%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CATGTCACATGATGA 20  
|||||  
Db 1 CATGTCACATGATGA 17  
RESULT 7  
ADT78880  
ID ADT78880 standard; DNA; 20 BP.  
XX  
AC ADT78880;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Antisense oligonucleotide (ISIS 337223) for human HIF1alpha/HIF2alpha.  
XX  
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;  
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;  
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;  
KW eye disorder; tumor; hyperplasia; pulmonary fibrosis; angiogenesis;  
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;  
KW blood vessel; restenosis; angioplasty; cyostatic; angiogenesis;  
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 12  
FT /\*tag= a  
FT /mod\_base= 1  
FT modified\_base 15  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= Pseudouridine"  
XX  
PN US2004220393-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 21-NOV-2003; 2003US-00719370.  
XX  
PR 23-NOV-2002; 2002US-00304126.  
XX  
PA (WARD/) WARD D T.  
PA (DOB1/) DOBIE K W.  
PA (MARC/) MARCUSON E G.  
PA (FRET/) FREIER S M.  
XX  
PI Ward DT, Dobie KW, Marcuson EG, Freier SM;  
XX WPI; 2004-774955/76.  
XX  
PT New antisense compound which inhibits the expression of hypoxia-inducible  
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating  
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.  
XX  
PS Example 30; SEQ ID NO 451; 195bp; English.  
XX  
CC The present invention relates to antisense compounds targeted to nucleic  
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or

CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound  
CC comprises an antisense oligonucleotide that specifically hybridizes with  
CC the nucleic acid and inhibits the expression of HIF1alpha and/or  
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.  
CC The antisense oligonucleotide comprises at least one modified  
CC internucleoside linkage, preferably a phosphorothioate linkage. It also  
CC comprises at least one modified sugar moiety, preferably a 2'-O-  
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further  
CC comprises at least one modified nucleobase, preferably a 5-  
CC methylcytosine. The antisense oligonucleotides are useful for the  
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,  
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder  
CC that affects the eye. The compound is also useful for treating tumors,  
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,  
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels  
CC such as stenosis or restenosis following angioplasty. It is also useful  
CC in drug discovery and target validation, and can be utilized for  
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
CC The present sequence represents an oligonucleotide used in the examples  
CC of the present invention.  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 2 Other;  
Query Match 85.0%; Score 17; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 5.1;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCTCATGTCACATGATG 19  
|||||  
Db 2 CCTCATGTCACATGATG 20  
RESULT 8  
ADT78872  
ID ADT78872 standard; DNA; 20 BP.  
XX  
AC ADT78872;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Antisense oligonucleotide (ISIS 330460) for human HIF2alpha.  
XX  
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;  
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;  
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;  
KW eye disorder; tumor; hyperplasia; pulmonary fibrosis; angiogenesis;  
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;  
KW blood vessel; restenosis; angioplasty; cyostatic; angiogenesis;  
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004220393-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 21-NOV-2003; 2003US-00719370.  
XX  
PR 23-NOV-2002; 2002US-00304126.  
XX  
PA (WARD/) WARD D T.  
PA (DOB1/) DOBIE K W.  
PA (MARC/) MARCUSON E G.  
PA (FRET/) FREIER S M.  
XX  
PI Ward DT, Dobie KW, Marcuson EG, Freier SM;  
XX WPI; 2004-774955/76.  
XX  
PT New antisense compound which inhibits the expression of hypoxia-inducible  
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating  
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.  
XX

PS Claim 92; SEQ ID NO 443; 195bp; English.

XX The present invention relates to antisense compounds targeted to nucleic  
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or  
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound  
CC comprises an antisense oligonucleotide that specifically hybridises with  
CC the nucleic acid and inhibits the expression of HIF1alpha and/or  
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.  
CC The antisense oligonucleotide comprises at least one modified  
CC internucleoside linkage, preferably a phosphorothioate linkage. It also  
CC comprises at least one modified sugar moiety, preferably a 2'-O-  
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further  
CC comprises at least one modified nucleobase, preferably a 5-  
CC methylcytosine. The antisense oligonucleotides are useful for the  
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,  
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder  
CC that affects the eye. The compound is also useful for treating tumours,  
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,  
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels  
CC such as stenosis or restenosis following angioplasty. It is also useful  
CC in drug discovery and target validation, and can be utilised for  
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
CC The present sequence represents an oligonucleotide used in the examples  
CC of the present invention.

XX  
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 5.5;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATGATGA 20  
DB 1 CCTCATGTCACATGATGA 20

RESULT 9  
ADT78877 standard; DNA; 20 BP.

XX  
AC ADT78877;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Antisense oligonucleotide (ISIS 330452) for human HIF1alpha.  
XX  
XX Antisense therapy; human; hypoxia-inducible factor 1 alpha;  
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;  
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;  
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;  
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;  
KW blood vessel; restenosis; angioplasty; cytoskeletal; angiogenesis;  
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004220393-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 21-NOV-2003; 2003US-00719370.  
XX  
PR 23-NOV-2002; 2002US-00304126.  
XX  
PA (WARD/) WARD D T.  
PA (DOB/) DOBIE K W.  
PA (MARC/) MARCUSSEN E G.  
PA (FRI/) FRIER S M.  
XX  
PI Ward DT, Dobie KW, Marcussen EG, Frier SM;  
XX  
DR WPI; 2004-774955/76.  
XX

PT New antisense compound which inhibits the expression of hypoxia-inducible  
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating  
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.

XX  
XX  
XX Claim 92; SEQ ID NO 448; 195bp; English.

XX The present invention relates to antisense compounds targeted to nucleic  
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or  
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound  
CC comprises an antisense oligonucleotide that specifically hybridises with  
CC the nucleic acid and inhibits the expression of HIF1alpha and/or  
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.  
CC The antisense oligonucleotide comprises at least one modified  
CC internucleoside linkage, preferably a phosphorothioate linkage. It also  
CC comprises at least one modified sugar moiety, preferably a 2'-O-  
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further  
CC comprises at least one modified nucleobase, preferably a 5-  
CC methylcytosine. The antisense oligonucleotides are useful for the  
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,  
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder  
CC that affects the eye. The compound is also useful for treating tumours,  
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,  
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels  
CC such as stenosis or restenosis following angioplasty. It is also useful  
CC in drug discovery and target validation, and can be utilised for  
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
CC The present sequence represents an oligonucleotide used in the examples  
CC of the present invention.

XX  
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATG 16  
DB 5 CCTCATGTCACATG 20

RESULT 10  
ADT78879 standard; DNA; 20 BP.

XX  
AC ADT78879;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Antisense oligonucleotide (ISIS 326743) for human HIF2alpha.  
XX  
XX Antisense therapy; human; hypoxia-inducible factor 1 alpha;  
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;  
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;  
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;  
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;  
KW blood vessel; restenosis; angioplasty; cytoskeletal; angiogenesis;  
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004220393-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 21-NOV-2003; 2003US-00719370.  
XX  
PR 23-NOV-2002; 2002US-00304126.  
XX  
PA (WARD/) WARD D T.  
PA (DOB/) DOBIE K W.  
PA (MARC/) MARCUSSEN E G.  
PA (FRI/) FRIER S M.  
XX  
PI  
XX  
DR

PI Ward DT, Dobie KM, Marcusson EG, Freier SM;  
XX  
XX WPI; 2004-774955/76.  
XX  
XX New antisense compound which inhibits the expression of hypoxia-inducible  
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating  
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.  
XX  
XX Claim 92; SEQ ID NO 450; 195bp; English.  
XX  
XX The present invention relates to antisense compounds targeted to nucleic  
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or  
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound  
CC comprises an antisense oligonucleotide that specifically hybridizes with  
CC the nucleic acid and inhibits the expression of HIF1alpha and/or  
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.  
CC The antisense oligonucleotide comprises at least one modified  
CC internucleoside linkage, preferably a phosphorothioate linkage. It also  
CC comprises at least one modified sugar moiety, preferably a 2'-O-  
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further  
CC comprises at least one modified nucleobase, preferably a 5-  
CC methylcytosine. The antisense oligonucleotides are useful for the  
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,  
CC that affects the eye. The compound is also useful for treating tumours,  
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,  
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels  
CC such as stenosis or restenosis following angioplasty. It is also useful  
CC in drug discovery and target validation, and can be utilized for  
CC diagnostics, therapeutic, prophylaxis and as research reagents and kits.  
CC The present sequence represents an oligonucleotide used in the examples  
CC of the present invention.  
XX  
XX Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 7.9;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATGATG 19  
|||  
DB 2 CCTCATGTCGACGAGATG 20

## RESULT 11

AAV13322 standard; DNA; 19 BP.

AAV13322;

14-MAY-1998 (first entry)

Sense primer Exon 4 for human 5-lipoxygenase gene.

Inflammatory disease; polymorphism; 5-lipoxygenase; asthma;  
KM ulcerative colitis; bronchitis; sinusitis; psoriasis; rhinitis;  
KM arthritis; diagnosis; treatment; PCR primer; ss.

Synthetic.

Homo sapiens.

WO9742347-A2.

13-NOV-1997.

29-APR-1997; 97MO-US007137.

06-MAY-1996; 96US-0016890P.

25-APR-1997; 97US-00846020.

(BGM) BRIGHAM & WOMEN'S HOSPITAL.

Drazen JM, In K, Asano K, Beier D, Grobholz J;

XX  
XX WPI; 1997-558997/51.  
XX  
XX Classifying patients with inflammatory disease, specifically asthma -  
PT according to polymorphisms in 5-lipoxygenase gene regulatory region, e.g.  
PT to identify candidates for lipoxygenase inhibitor treatment.  
XX  
XX Example 1; Page 19; 56bp; English.  
XX

The present sequence was used in the development of a novel method for  
CC classifying patients suffering from an inflammatory disease. The method  
CC comprises identifying in DNA from at least 1 patient a sequence  
CC polymorphism, as compared with the normal 5-lipoxygenase (5-LOX) gene  
CC (AAT88431), in a 5-LOX regulatory gene sequence. The method can be  
CC applied to subjects with asthma, ulcerative colitis, bronchitis,  
CC sinusitis, psoriasis, allergic and non-allergic rhinitis, lupus or  
CC rheumatoid arthritis. Specifically it can be used to diagnose asthma or  
CC susceptibility to disease, identify treatments suitable for individual  
CC patients or assess the likely success of treatment  
XX

Sequence 19 BP; 4 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTCATGTCACATGATG 19  
|||  
DB 2 CTCATGTCACATGATG 19

## RESULT 12

ADZ58131 standard; RNA; 19 BP.

ADZ58131;

30-JUN-2005 (first entry)

Antisense siRNA oligo that modulates human HIF1 expression Seq 259.

ss; short interfering RNA; siRNA; gene silencing; RNA interference;  
KM hypoxia inducible factor 1; cancer; hyperproliferation;  
KM macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;  
KM anti-diabetic; antisense.

Homo sapiens.

WO2005035759-A2.

21-APR-2005.

20-AUG-2004; 2004MO-US027294.

20-AUG-2003; 2003US-0496655P.

23-OCT-2003; 2003US-00693059.

24-NOV-2003; 2003US-00720448.

03-DEC-2003; 2003US-00727780.

14-JAN-2004; 2004US-00757803.

10-FEB-2004; 2004US-0543480P.

13-FEB-2004; 2004US-00780447.

16-APR-2004; 2004US-00826966.

30-APR-2004; 54US-09997777.

24-MAY-2004; 54US-09996666.

(SIRN-) SIRNA THERAPEUTICS INC.

Usman N, Mcswigen J;

WPI; 2005-306364/31.

New chemically synthesized double stranded short interfering nucleic acid  
PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via

PT RNA interference (RNAi), useful for modulating HIF1, its expression or  
 PT activity.  
 PS Claim 33; SEQ ID NO 259; 1899p; English.  
 XX  
 XX This invention relates to a novel chemically synthesized double stranded  
 CC short interfering nucleic acid strand (siRNA). Specifically, it refers to  
 CC siRNA that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via  
 CC RNA interference (RNAi). In particular, the siRNA may include short  
 CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)  
 CC and short hairpin RNA (shRNA) molecules that are capable of mediating  
 CC RNAi. The present invention describes a sense strand of a double-stranded  
 CC siRNA that comprises a nucleotide sequence that is complementary to HIF1  
 CC RNA or a portion thereof, and where a second strand is the complementary  
 CC antisense siRNA strand. Note that the sense region is connected to the  
 CC antisense region via a polynucleotide linker molecule. Accordingly, these  
 CC siRNA are useful in providing compositions for the treatment of trials,  
 CC diseases and conditions that respond to modulation of HIF1 expression,  
 CC namely cancer and proliferative conditions including macular  
 CC degeneration, diabetic retinopathy and other conditions associated with  
 CC hypoxia inducible proliferation. As such, these compositions exhibit  
 CC cytostatic, ophthalmological and antidiabetic activities. This  
 CC oligonucleotide sequence is an antisense siRNA strand that targets human  
 CC HIF1 RNA to modulate expression given in an exemplification of the  
 CC invention.  
 XX  
 XX Sequence 19 BP; 7 A; 2 C; 6 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 70.0%; Score 14; DB 1; Length 19;  
 Best Local Similarity 78.6%; Pred. No. 13;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GGTCACTGGATGA 20  
 DB 1 GGUCAACUGAUGA 14  
 ||:||||:||||:  
 RESULT 13  
 AD257911/c  
 ID AD257911 standard; RNA; 19 BP.  
 XX  
 XX AD257911;  
 AC  
 XX  
 XX 30-JUN-2005 (first entry)  
 DT  
 XX  
 XX Sense siRNA oligo that modulates human HIF1 expression Seq 39.  
 DE  
 XX  
 XX ss; short interfering RNA; siRNA; gene silencing; RNA interference;  
 KW hypoxia inducible factor 1; cancer; hyperproliferation;  
 KW macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;  
 KW antidiabetic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2005035759-A2.  
 PN  
 XX  
 XX 21-APR-2005.  
 PD  
 XX  
 XX 20-AUG-2004; 2004WO-US027294.  
 PF  
 XX  
 XX 20-AUG-2003; 2003US-0496655P.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 54US-08997777.  
 PR 24-MAY-2004; 54US-09996666.  
 XX  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA  
 XX

PI Usman N, Mcswigen U;  
 XX  
 XX WPI; 2005-306364/31.  
 DR  
 XX  
 XX New chemically synthesized double stranded short interfering nucleic acid  
 PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via  
 PT RNA interference (RNAi), useful for modulating HIF1, its expression or  
 PT activity.  
 PS Claim 33; SEQ ID NO 39; 1899p; English.  
 XX  
 XX This invention relates to a novel chemically synthesized double stranded  
 CC short interfering nucleic acid strand (siRNA). Specifically, it refers to  
 CC siRNA that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via  
 CC RNA interference (RNAi). In particular, the siRNA may include short  
 CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)  
 CC and short hairpin RNA (shRNA) molecules that are capable of mediating  
 CC RNAi. The present invention describes a sense strand of a double-stranded  
 CC siRNA that comprises a nucleotide sequence that is complementary to HIF1  
 CC RNA or a portion thereof, and where a second strand is the complementary  
 CC antisense siRNA strand. Note that the sense region is connected to the  
 CC antisense region via a polynucleotide linker molecule. Accordingly, these  
 CC siRNA are useful in providing compositions for the treatment of trials,  
 CC diseases and conditions that respond to modulation of HIF1 expression,  
 CC namely cancer and proliferative conditions including macular  
 CC degeneration, diabetic retinopathy and other conditions associated with  
 CC hypoxia inducible proliferation. As such, these compositions exhibit  
 CC cytostatic, ophthalmological and antidiabetic activities. This  
 CC oligonucleotide sequence is a sense siRNA strand that targets human HIF1  
 CC RNA to modulate expression given in an exemplification of the invention.  
 XX  
 XX Sequence 19 BP; 4 A; 6 C; 2 G; 0 T; 7 U; 0 Other;  
 SQ  
 Query Match 70.0%; Score 14; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GGTCACTGGATGA 20  
 DB 19 GGTCACTGGATGA 6  
 |||||  
 RESULT 14  
 ABR38435/c  
 ID ABR38435 standard; DNA; 17 BP.  
 XX  
 XX ABR38435;  
 AC  
 XX  
 XX 12-JUN-2003 (first entry)  
 DT  
 XX  
 XX Tumour suppression related human fukutin oligo SEQ ID No 4072.  
 DE  
 XX  
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2003025175-A2.  
 PN  
 XX  
 XX 27-MAR-2003.  
 PD  
 XX  
 XX 17-SEP-2002; 2002WO-1B004208.  
 PR 17-SEP-2001; 2001FR-00011978.  
 PR  
 XX  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA  
 XX  
 XX Telerman A, Amson R, Tuijnder M;  
 PI  
 XX  
 XX WPI; 2003-313353/30.  
 DR  
 XX

PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
XX disclosure, Page 510; 720pp; French.  
XX  
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
XX Sequence 17 BP; 4 A; 4 C; 3 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 64.0%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 16;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 TCATGTCACATGATG 18  
DB 17 TCAGGCTCAATGAT 2  
RESULT 15  
ADM14071/c  
ID ADM14071 standard; DNA; 18 BP.  
XX  
XX ADM14071;  
XX  
XX 07-APR-2005 (first entry)  
XX  
XX KCMNA1 exon 1B sense PCR primer, SEQ ID 3.  
XX  
XX KCMNA1 exon 1B sense PCR primer, SEQ ID 3.  
XX  
XX Noctropic; autism; potassium channel; KCMNA1; PCR; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX FR2657452-A1.  
XX  
XX 14-JAN-2005.  
XX  
XX 11-JUL-2003; 2003FR-00008527.  
XX  
XX 11-JUL-2003; 2003FR-00008527.  
XX  
XX 11-JUL-2003; 2003FR-00008527.  
XX  
XX (UYRA-) UNIV RABBITAIS FRANCOIS.  
XX  
XX Briault S, Laumonier F, le Guennec JY, Roger S;  
XX  
XX MPI; 2005-114499/13.  
XX  
XX Test for identifying autism, comprises detecting reduction in activity of  
PT calcium-dependent potassium channels by measuring the electrical activity  
PT of the channels.  
XX  
XX Example 1; SEQ ID NO 3; 42pp; French.  
XX  
XX

XX  
CC The present invention relates to a test for detecting autism, which  
CC comprises measuring the electrical activity of calcium-dependent  
CC potassium channels (BKCa) in a sample of blood cells and detecting any  
CC reduction in activity, relative to a control sample. Also claimed are:  
CC selecting a subpopulation of patients with autism by performing the new  
CC method and selecting subjects with reduced BKCa activity; and use of  
CC activators or agonists of BKCa to prepare a composition for treating  
CC autism where this is associated with deficient electrical activity. The  
CC method is useful for autism diagnosis and prognosis and to identify a  
CC subset of autism patients who may benefit from treatment with activators  
CC or agonists (X) of BKCa, i.e. patients where autism is linked to a  
CC defective electrical activity. In an example from the invention, a  
CC translocation in the potassium channel KCMNA1 gene in a six year old  
CC patient with autism was detected and characterized using PCR primers  
CC ADM14069-ADM14128. The KCMNA1 gene encodes a protein of the glutamatergic  
CC complex, and mutation of the KCMNA1 gene resulting in inadequate  
CC functioning of BKCa. The translocation was (46, XY, t(9;10)(q23;q22)),  
CC and the break was between the first and second exons of the KCMNA1 gene  
CC and amplification tests showed that, in the patient, one copy of the  
CC KCMNA1 was inactivated.  
XX  
XX Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 64.0%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 18;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 CATGTCACATGATG 19  
DB 16 CATGTCACCGGATG 1  
RESULT 16  
ABN07620/c  
ID ABN07620 standard; DNA; 17 BP.  
XX  
XX ABN07620;  
XX  
XX 29-MAY-2002 (first entry)  
XX  
XX Human GMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7612.  
XX  
XX Human; genome-derived myosin-like protein 1; GMLP-1; heart;  
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192524-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 25-MAY-2001; 2001WO-US016981.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX  
XX 21-SEP-2000; 2000US-0234687P.  
XX  
XX 27-SEP-2000; 2000US-0236359P.  
XX  
XX 04-OCT-2000; 2000GB-00024263.  
XX  
XX 30-JAN-2001; 2001WO-US000662.  
XX  
XX 30-JAN-2001; 2001WO-US000662.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX  
XX 30-JAN-2001; 2001WO-US000664.  
XX  
XX 30-JAN-2001; 2001WO-US000665.  
XX  
XX 30-JAN-2001; 2001WO-US000666.  
XX  
XX 30-JAN-2001; 2001WO-US000667.  
XX  
XX 30-JAN-2001; 2001WO-US000668.  
XX  
XX 30-JAN-2001; 2001WO-US000669.  
XX  
XX 30-JAN-2001; 2001WO-US000670.  
XX  
XX 05-FEB-2001; 2001US-0266860P.  
XX  
XX (ABOM-) AEOMICA INC.  
XX  
XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPL-1.  
XX  
PS Disclosure; SEQ ID NO 7612; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPL-1  
CC expressing the proteins. The hGDMPL-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPL  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPL proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPL-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPL-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPL-1, in particular heart  
CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 20;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTCATGTCACATGCA 17  
DB 17 CCTCAAGTCACAGGTA 1

RESULT 17  
ACN12001  
ID ACN12001 standard; RNA; 17 BP.  
XX  
XX ACN12001;  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX MNV minus strand Inozyme substrate SEQ ID NO 12004.  
DE  
XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
XX viroicide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyne; ss.  
XX  
XX West Nile Virus.  
OS  
XX  
XX MO20026637-A2.  
PN  
XX  
PD 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
PF  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
PR  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT) BLATT L.  
PA (MCSW/) MCSWIGEN J A.

XX  
XX Blatt L, Mcswigen JA;  
PI  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNV), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX  
PS Claim 23; SEQ ID NO 12004; 495pp; English.

XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-leaver, DNAzyme, Amberzyme and Zinzyne. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX

SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 20;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 TCATGTCACATGATG 19  
DB 1 UCACUCUCACAGCAUG 17

RESULT 18  
ACN70710/C  
ID ACN70710 standard; DNA; 17 BP.

XX  
XX ACN70710;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
XX Human GDMPL-1 probe SEQ ID NO:7612.  
DE  
XX Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
XX hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
XX skeletal muscle function.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2004137589-A1.  
PN  
XX  
PD 15-JUL-2004.  
XX  
XX 26-NOV-2003; 2003US-00723361.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 PA (GUTY/) GU Y.  
 PI (CITY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 PI Gu Y, JI Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 DR WPI; 2004-533378/51.  
 XX  
 PT Novel myosin-like protein-1, useful for treating or preventing disorder  
 associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 7612; 0pp; English.  
 XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMMP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
 CC antagonist of hGDMMP-1, or as an inhibitor of hGDMMP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMMP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 61.0%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 20;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CCTCATGCTCATGGA 17  
 DB 17 CCTCAAGTCACAGGTA 1  
 RESULT 19  
 AAF51883/c  
 ID AAF51883 standard; DNA; 15 BP.  
 XX  
 AC AAF51883;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-1 oligonucleotide #2843.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.

XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 79; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, ptyriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 59.0%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 18;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 TGGTCACGATGGA 20  
 DB 15 TATTCAGATGATGA 1  
 RESULT 20  
 AAF51884/c  
 ID AAF51884 standard; DNA; 15 BP.  
 XX  
 AC AAF51884;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-1 oligonucleotide #2844.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;

XX  
DR WPI; 2001-041421/05.  
XX  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
PS Example 8; Page 79; 201pp; English.  
XX  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, seborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 59.0%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 18;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 ATGGTCACATGATG 19  
DB 15 ATGATCAGATGATG 1  
XX  
RESULT 21  
AD259539/c  
ID AD259539 standard; DNA; 16 BP.  
XX  
XX AD259539;  
AC  
XX  
DT 30-JUN-2005 (first entry)  
DE Hyperparathyroidism polymorphic detection VIC probe, SEQ ID 33.  
XX  
XX secondary hyperparathyroidism; endocrine-gen.; antihypoid;  
KM renal failure; nephrotropic; SNP detection; ss; probe.  
XX  
XX Synthetic.  
XX  
XX JP2005102601-A.  
PN  
XX  
PD 21-APR-2005.  
XX  
PF 30-SEP-2003; 2003JP-00341015.  
XX  
PR 30-SEP-2003; 2003JP-00341015.  
XX  
XX (HYUB-) HYBITTO GENOMICS KK.  
PA (JIKE-) UNIV JIKEI.  
XX  
XX WPI; 2005-358641/37.  
DR  
XX  
XX Testing secondary hyperparathyroidism in chronic renal failure patient,  
PT involves detecting variation in gene chosen from CACNA1C, CALCR1, CH13L1,  
PT EGF, FGFR1, GFRAL, GPR56 and GPRK6.  
XX  
XX  
PS Disclosure; SEQ ID NO 33; 138pp; Japanese.  
XX  
XX The invention relates to a novel method for testing secondary  
CC hyperparathyroidism in a chronic renal failure patient. The method

CC involves detecting a variation in a gene chosen from CACNA1C, CALCR1,  
CC CH13L1, EGF, FGFR1, GFRAL, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,  
CC KCNQ1, ORCT14, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,  
CC IL17R, OSTF1, FGF6, HGF, MET, TGFBI and VEGF, or detecting the base in a  
CC polymorphism region existing in the vicinity of any one of the genes. The  
CC invention further comprises a reagent or kit for testing secondary  
CC hyperparathyroidism in a chronic renal failure patient. This  
CC polynucleotide sequence represents a probe used in the detection of a  
CC polymorphism in a gene linked to secondary hyperparathyroidism of the  
CC invention.  
XX  
SQ Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 59.0%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 20;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 TCATGGTCACATGCA 17  
DB 16 TCTTGCTCACAGCA 2  
XX  
RESULT 22  
AD259706/c  
ID AD259706 standard; DNA; 16 BP.  
XX  
XX AD259706;  
AC  
XX  
DT 30-JUN-2005 (first entry)  
DE Hyperparathyroidism polymorphic detection VIC probe, SEQ ID 200.  
XX  
XX secondary hyperparathyroidism; endocrine-gen.; antihypoid;  
KM renal failure; nephrotropic; SNP detection; ss; probe.  
XX  
XX Synthetic.  
XX  
XX JP2005102601-A.  
PN  
XX  
PD 21-APR-2005.  
XX  
PF 30-SEP-2003; 2003JP-00341015.  
XX  
PR 30-SEP-2003; 2003JP-00341015.  
XX  
XX (HYUB-) HYBITTO GENOMICS KK.  
PA (JIKE-) UNIV JIKEI.  
XX  
XX WPI; 2005-358641/37.  
DR  
XX  
XX Testing secondary hyperparathyroidism in chronic renal failure patient,  
PT involves detecting variation in gene chosen from CACNA1C, CALCR1, CH13L1,  
PT EGF, FGFR1, GFRAL, GPR56 and GPRK6.  
XX  
XX  
PS Disclosure; SEQ ID NO 200; 138pp; Japanese.  
XX  
XX The invention relates to a novel method for testing secondary  
CC hyperparathyroidism in a chronic renal failure patient. The method  
CC involves detecting a variation in a gene chosen from CACNA1C, CALCR1,  
CC CH13L1, EGF, FGFR1, GFRAL, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,  
CC KCNQ1, ORCT14, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,  
CC IL17R, OSTF1, FGF6, HGF, MET, TGFBI and VEGF, or detecting the base in a  
CC polymorphism region existing in the vicinity of any one of the genes. The  
CC invention further comprises a reagent or kit for testing secondary  
CC hyperparathyroidism in a chronic renal failure patient. This  
CC polynucleotide sequence represents a probe used in the detection of a  
CC polymorphism in a gene linked to secondary hyperparathyroidism of the  
CC invention.  
XX  
SQ Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 59.0%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 20;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCATGGTCACATGGA 17  
16 TCTTGGTCACAGGGA 2

## RESULT 23

ADG13603  
ID ADG13603 standard; RNA; 15 BP.

AC ADG13603;

XX 26-FEB-2004 (first entry)

DE Human HERR1-4 hammerhead ribozyme target sequence #3.

XX Human; ss; EGFR; epidermal growth factor receptor; HERR1; HERR2; HERR3;  
KM HERR4; hammerhead ribozyme; inozyme; zinzyme; DNazyme; amberzyme; cancer;  
KM brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;  
KM prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;  
KM stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;  
KM head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;  
KM multidrug resistant cancer.

XX Homo sapiens.

PN US2003186909-A1.

PD 02-OCT-2003.

PF 21-OCT-2002; 2002US-00277494.

XX 27-JAN-1997; 97US-0036749P.

PR 04-DEC-1997; 97US-00985162.

PR 22-SEP-1999; 99US-00401063.

PR 03-MAY-2001; 2001US-00848754.

PR 25-JUL-2001; 2001US-00916466.

XX (RIBO-) RIBOZYME PHARM INC.

PI Mcswiggen J;

DR WPI; 2004-032029/03.

XX New double stranded short interfering ribonucleic acid molecule for  
inhibiting expression of epidermal growth factor receptor gene.

PS Claim 7; SEQ ID NO 30; 113pp; English.

XX The invention relates to a double stranded short interfering RNA (siRNA)  
molecule that inhibits expression of epidermal growth factor receptor  
(EGFR) gene (e.g. HERR1-4) by RNA interference is new. Also included is an  
expression vector comprising a nucleic acid sequence encoding siRNA  
molecule(s) in a manner that allows expression of the nucleic acid  
molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,  
amberzymes, zinzymes and DNazymes. The invention is used for inhibiting  
expression of EGFR. It can be used for treatment of cancer, prostate  
cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach  
cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck  
cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant  
cancer or a brain tumour. The invention has enhanced shelf-life, half-  
life in vitro, stability, and ease of introduction of oligonucleotide to  
target site. The present sequence is an EGFR/HERR1-4 target sequence for  
an siRNA of the invention.

XX Sequence 15 BP; 4 A; 2 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 1; Length 15;

Best Local Similarity 61.5%; Pred. No. 21;  
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGGTCACATG 15

Db :||:|:|:|:|:|  
1 UCAUGGUCAAUG 13

## RESULT 24

ADM69289/C  
ID ADM69289 standard; DNA; 16 BP.

AC ADM69289;

XX 03-JUN-2004 (first entry)

DE Plant gene polymorphism marker related primer, SEQ ID 168.

XX Primer; variation mapping; mutation mapping; plant;

KM gene polymorphism marker; ss.

XX Synthetic.

XX JP2003289885-A.

PN 14-OCT-2003.

PF 31-JAN-2003; 2003JP-00024620.

XX 01-FEB-2002; 2002JP-00025338.

XX (RIKA) RIKAGAKU KENKYUSHO.

PA (SAIM-) SAI MEDIA KK.

PA (MATS/) MATSUI M.

PA (NAKA/) NAKAZAWA M.

XX WPI; 2004-126231/13.

PT A primer set and method useful for mapping at least the  
variation/mutation part of a plant gene using a gene polymorphism marker.

XX The present invention relates to a primer set and method for mapping at  
least the variation/mutation part of a plant gene using a gene  
polymorphism marker. A mutation site of the plant gene is mapped by  
utilizing a genetic polymorphism marker as follows: (a) genomic DNA is  
prepared from a plant homozygously having a mutation to be an object of  
the mapping; (b) A forward primer 1 containing a base corresponding to  
the gene polymorphic marker of one ecotype plant, a forward primer 2  
containing a base corresponding to the genetic polymorphism of the other  
ecotype plant and a reverse primer 3 based on the base sequence common  
with both the ecotype plants are prepared; (c) two kinds of  
oligonucleotides emitting fluorescence of different colors when the  
CC genetic polymorphism marker is detected are prepared; (d) an  
amplification reaction of the genomic DNA is carried out in the presence  
of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)  
the fluorescence intensity emitted from the resultant reaction product  
is detected and (f) the position on the genome of the mutation site is  
determined from the results of detection. The present sequence is a  
primer, used to illustrate the invention.

XX Sequence 16 BP; 2 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 23;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GTCACATGGATGA 20

Db 14 GTCACATGGAGGA 2

## RESULT 25

ADR74253/C  
ID ADR74253 standard; DNA; 16 BP.

XX

AC ADR74253;  
XX  
XX 16-DEC-2004 (first entry)  
DT  
XX  
XX Common primer B for human MI-associated marker hcv2633049.  
DE  
XX  
XX Human; ss; PCR; primer; SNP; single nucleotide polymorphism;  
KM myocardial infarction.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004081187-A2.  
PN  
XX  
XX 23-SEP-2004.  
PD  
XX  
XX 10-MAR-2004; 2004WO-US007141.  
PF  
XX  
XX 10-MAR-2003; 2003US-0453135P.  
PR 30-APR-2003; 2003US-0466412P.  
XX  
XX (APPL-) APPLERA CORP.  
PA  
XX  
XX Cargill M, Devlin JJ, Iakubova O, Shiffman D;  
PI  
XX  
XX MPI; 2004-677537/66.  
DR  
XX  
XX Identifying an individual who has altered risk for developing myocardial  
PT infarction comprises detecting single nucleotide polymorphism (SNP), in  
PT the individual's nucleic acids.  
XX  
XX  
XX Claim 19; SEQ ID NO 44078; 139p; English.  
PS  
XX  
XX The invention relates to identifying an individual who has altered risk  
CC for developing myocardial infarction comprising detecting single  
CC nucleotide polymorphism (SNP) in any one of the 43336 nucleotide  
CC sequences (not given in the specification), in the individual's nucleic  
CC acids, where the presence of the SNP is correlated with an altered risk  
CC for myocardial infarction in the individual. Also included are an  
CC isolated nucleic acid molecule (comprising at least 8 contiguous  
CC nucleotides where one of the nucleotides is an SNP as cited above, or  
CC their complement), an isolated polypeptide comprising an amino acid  
CC sequence selected from any of the 696 amino acid sequences not defined in  
CC the specification, an antibody that specifically binds to the polypeptide  
CC (or its antigen-binding fragment), an amplified polynucleotide containing  
CC the SNP as cited (where the amplified polynucleotide is between about 16  
CC and about 1,000 nucleotides in length), an isolated polynucleotide which  
CC specifically hybridizes to a nucleic acid molecule containing the SNP, a  
CC kit for detecting SNP in a nucleic acid, detecting SNP in a nucleic acid  
CC molecule, detecting a variant polypeptide and identifying an agent useful  
CC in therapeutically or prophylactically treating myocardial infarction.  
CC The detection step of the method is carried out by a process selected  
CC from allele-specific probe hybridization, allele-specific primer  
CC extension, allele-specific amplification, sequencing, 5' nuclease  
CC digestion, molecular beacon assay, oligonucleotide ligation assay, size  
CC analysis, and single-stranded conformation polymorphism. The method is  
CC useful for identifying an individual who has altered risk for developing  
CC myocardial infarction. The present sequence is common primer (used with  
CC an allele specific PCR primer) used to amplify an SNP-containing region  
CC from a myocardial infarction-associated marker gene. NOTE: SEQ IDs 1-  
CC 43787 are not shown in the specification and are not available from WIPO.  
CC These sequence are contained on a CD-R named CL001509CDR which has not  
CC been supplied with the specification.  
XX  
XX  
SQ Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 56.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 25;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CTTGATGTCACATCG 16  
DB 16 CTTGATGTCACATCG 16

RESULT 26  
ABK09404  
ID ABK09404 standard; DNA; 15 BP.  
XX  
XX  
XX ABK09404;  
AC  
XX  
XX 14-MAR-2002 (first entry)  
DT  
XX  
XX Human NRP1 gene allele-specific oligonucleotide sequencing primer #26.  
DE  
XX  
XX Human; natriuretic peptide receptor A/guanylate cyclase A; NRP1; ss;  
KM atrionatriuretic peptide receptor A; haplotyping; cytosatic; genotyping;  
KM haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;  
KM drug screening; hypertension; hypotensive; sequencing primer; probe.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200179231-A2.  
PN  
XX  
XX 25-OCT-2001.  
PD  
XX  
XX 16-APR-2001; 2001WO-US012300.  
PF  
XX  
XX 14-APR-2000; 2000US-0197330P.  
PR  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX  
XX Bentivegna SC, Choi JY, Klem SE, Nandabalan K;  
PI  
XX  
XX MPI; 2002-066340/09.  
DR  
XX  
XX Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of  
PT an individual, involves determining identity of nucleotide pair at  
PT specific polymorphic sites for two copies of the gene.  
XX  
XX  
XX Claim 15; Page 14; 96p; English.  
PS  
XX  
XX The invention relates to single nucleotide polymorphisms in the gene  
CC encoding the human natriuretic peptide receptor A/guanylate cyclase A  
CC (atrionatriuretic peptide receptor A) or NRP1 polypeptide. A method for  
CC haplotyping the NRP1 gene in an individual comprises identifying the  
CC nucleotide at one or more polymorphic sites and determining whether one  
CC of the copies of the gene is defined by one of the NRP1 haplotypes given  
CC in the specification or whether both copies are defined by a haplotype  
CC pair. This method is useful in genotyping, whereby all possible haplotype  
CC pairs can be assigned to specific genotypes. An association between a  
CC trait and a haplotype or haplotype pair of the NRP1 gene can be  
CC identified by comparing the frequency of the haplotype or haplotype pair  
CC in a population exhibiting the trait with the frequency of the haplotype  
CC or haplotype pair in a reference population, where a higher haplotype  
CC frequency in the trait population indicates the trait is associated with  
CC the haplotype or haplotype pair. NRP1 and its corresponding DNA are used  
CC for studying the expression and function of NRP1, for use in screening  
CC for candidate drugs to treat diseases related to NRP1 activity, such as  
CC hypertension. The sequences are also useful for studying the effect of  
CC variation on the biological activity of NRP1 as well as on the binding  
CC affinity of candidate drugs targeting NRP1. Sequences AAS9959-AAS9990  
CC and ABK09390-ABK09462 represent probes, sequencing primers and PCR  
CC primers used to detect NRP1 gene polymorphisms  
XX  
XX  
SQ Sequence 15 BP; 5 A; 4 C; 3 G; 2 T; 0 U; 1 Other;  
Query Match 55.0%; Score 11; DB 1; Length 15;  
Best Local Similarity 84.6%; Pred. No. 24;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CTCATGTCACAT 14  
DB 2 CTCATGTCACAT 14

RESULT 27

ACL73850  
 ID ACL73850 standard; DNA; 15 BP.  
 AC ACL73850;  
 DT 16-JUN-2005 (first entry)  
 DE SARS coronavirus right PCR primer, SEQ:631.  
 KM Vaccine; nucleic acid vaccine; drug screening; diagnosis;  
 KM SARS coronavirus infection; infection; respiratory disease; virucide;  
 KM PCR; primer; ss.  
 OS SARS coronavirus.  
 PN WO2004092360-A2.  
 PD 28-OCT-2004.  
 PF 09-APR-2004; 2004WO-US011710.  
 PR 10-APR-2003; 2003US-0462218P.  
 PR 11-APR-2003; 2003US-0462465P.  
 PR 12-APR-2003; 2003US-0462418P.  
 PR 13-APR-2003; 2003US-0462748P.  
 PR 14-APR-2003; 2003US-0463109P.  
 PR 15-APR-2003; 2003US-0463460P.  
 PR 16-APR-2003; 2003US-0463668P.  
 PR 17-APR-2003; 2003US-0463981P.  
 PR 18-APR-2003; 2003US-0463971P.  
 PR 22-APR-2003; 2003US-0464838P.  
 PR 23-APR-2003; 2003US-0464899P.  
 PR 24-APR-2003; 2003US-0465273P.  
 PR 05-MAY-2003; 2003US-0465355P.  
 PR 22-MAY-2003; 2003US-0473144P.  
 PR 14-AUG-2003; 2003US-0495024P.  
 PR 23-SEP-2003; 2003US-0505552P.  
 PR 11-OCT-2003; 2003US-0510781P.  
 PR 11-DEC-2003; 2003US-0529464P.  
 PR 12-JAN-2004; 2004US-0536177P.  
 PR 07-APR-2004; 2004US-0560757P.  
 (CHIR ) CHIRON CORP.  
 PA Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;  
 PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JI;  
 PI Klenk HD, Valiante N;  
 XX MPI; 2004-766863/75.  
 DR Novel isolated polypeptide e.g. spike polypeptide, of  
 PT severe acute respiratory syndrome virus (SARS), useful as vaccine for  
 PT SARS.  
 PS Claim 59; SEQ ID NO 631; 839bp; English.  
 XX The invention relates to isolated polypeptides of the severe acute  
 CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike  
 CC (S or E2), env (E or SM), membrane (M or E1), hemagglutinin-esterase (HE  
 CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab  
 CC (replicase) polypeptides and their proteolytic fragments. The invention  
 CC also relates to antibodies which recognise the polypeptides; nucleic  
 CC acid encoding the SARS virus polypeptides; primers specific for SARS  
 CC virus nucleic acid sequences; kits for amplifying SARS virus target  
 CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length  
 CC which is able to inactivate the SARS virus in a mammalian cell; an  
 CC expression construct for recombinant expression of a SARS virus spike  
 CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-  
 CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS  
 CC viral antigen. The invention additionally provides a vaccine for the  
 CC treatment or prevention of SARS comprising an inactivated SARS virus, a  
 CC killed SARS virus, an attenuated SARS virus, a split SARS virus

CC preparation, or at least one purified SARS virus antigens; methods of  
 CC making inactivated SARS virus and vaccines containing it; an alpha-virus  
 CC replicon particle comprising one or more SARS viral antigens; and a  
 CC vaccine comprising one or more SARS virus antigens and one or more  
 CC respiratory virus antigens. The invention further encompasses a method of  
 CC identifying a therapeutically active agent by measuring the effect of the  
 CC agent on a SARS-related enzyme, and a method of treating a SARS patient  
 CC using small molecule viral inhibitors. The SARS virus polypeptides and  
 CC nucleic acids can be used in the preparation and manufacture of vaccines  
 CC for the treatment or prevention of SARS. The SARS virus polypeptides,  
 CC antibodies against them, and SARS virus-specific primers and kits  
 CC containing them are useful for diagnosing or identifying the presence of  
 CC SARS in a biological sample. The present sequence represents a PCR primer  
 CC for amplifying a SARS coronavirus gene. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SO Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 55.0%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTCATGTCAC 12  
 DB 5 CTCATGTCAC 15  
 RESULT 28  
 ID ACL73880 standard; DNA; 15 BP.  
 AC ACL73880;  
 XX  
 DT 16-JUN-2005 (first entry)  
 DE SARS coronavirus right PCR primer, SEQ:661.  
 KM Vaccine; nucleic acid vaccine; drug screening; diagnosis;  
 KM SARS coronavirus infection; infection; respiratory disease; virucide;  
 KM PCR; primer; ss.  
 OS SARS coronavirus.  
 PN WO2004092360-A2.  
 PD 28-OCT-2004.  
 PF 09-APR-2004; 2004WO-US011710.  
 PR 10-APR-2003; 2003US-0462218P.  
 PR 11-APR-2003; 2003US-0462465P.  
 PR 12-APR-2003; 2003US-0462418P.  
 PR 13-APR-2003; 2003US-0462748P.  
 PR 14-APR-2003; 2003US-0463109P.  
 PR 15-APR-2003; 2003US-0463460P.  
 PR 16-APR-2003; 2003US-0463668P.  
 PR 17-APR-2003; 2003US-0463981P.  
 PR 18-APR-2003; 2003US-0463971P.  
 PR 22-APR-2003; 2003US-0464838P.  
 PR 23-APR-2003; 2003US-0464899P.  
 PR 24-APR-2003; 2003US-0465273P.  
 PR 05-MAY-2003; 2003US-0465355P.  
 PR 22-MAY-2003; 2003US-0473144P.  
 PR 14-AUG-2003; 2003US-0495024P.  
 PR 23-SEP-2003; 2003US-0505552P.  
 PR 11-OCT-2003; 2003US-0510781P.  
 PR 11-DEC-2003; 2003US-0529464P.  
 PR 12-JAN-2004; 2004US-0536177P.  
 PR 07-APR-2004; 2004US-0560757P.  
 XX

PA (CHIR ) CHIRON CORP.  
 XX  
 PI Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J,  
 PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JF,  
 PI Klenk HD, Valiante N;  
 XX  
 DR WPI, 2004-766863/75.  
 XX  
 PT Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of  
 PT severe acute respiratory syndrome virus (SARS), useful as vaccine for  
 PT SARS.  
 XX  
 PS Claim 59; SEQ ID NO 661; 839pp; English.  
 XX  
 CC The invention relates to isolated polypeptides of the severe acute  
 CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike  
 CC (S or E2), env (E or SM), membrane (M or E1), hemagglutinin-esterase (HE  
 CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab  
 CC (replicase) polypeptides and their proteolytic fragments. The invention  
 CC also relates to antibodies which recognise the polypeptides; nucleic  
 CC acids encoding the SARS virus polypeptides; primers specific for SARS  
 CC virus nucleic acid sequences; kits for amplifying SARS virus target  
 CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length  
 CC which is able to inactivate the SARS virus in a mammalian cell; an  
 CC expression construct for recombinant expression of a SARS virus spike  
 CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-  
 CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS  
 CC viral antigen. The invention additionally provides a vaccine for the  
 CC treatment or prevention of SARS comprising an inactivated SARS virus, a  
 CC killed SARS virus, an attenuated SARS virus, a split SARS virus  
 CC preparation, or at least one purified SARS virus antigens; methods of  
 CC making inactivated SARS virus and vaccines containing it; an alpha-virus  
 CC replicon particle comprising one or more SARS virus antigens; and a  
 CC vaccine comprising one or more SARS virus antigens and one or more  
 CC respiratory virus antigens. The invention further encompasses a method of  
 CC identifying a therapeutically active agent by measuring the effect of the  
 CC agent on a SARS-related enzyme, and a method of treating a SARS patient  
 CC using small molecule viral inhibitors. The SARS virus polypeptides and  
 CC nucleic acids can be used in the preparation and manufacture of vaccines  
 CC for the treatment or prevention of SARS. The SARS virus polypeptides,  
 CC antibodies against them, and SARS virus-specific primers and kits  
 CC containing them are useful for diagnosing or identifying the presence of  
 CC SARS in a biological sample. The present sequence represents a PCR primer  
 CC for amplifying a SARS coronavirus gene. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published/pct\_sequences  
 XX  
 SQ Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 55.0%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTCATGCTCAC 12  
 Db 1 CTCATGCTCAC 11  
 RESULT 29  
 ACL73792  
 ID ACL73792 standard; DNA, 15 BP.  
 AC  
 AC ACL73792;  
 DT 16-JUN-2005 (first entry)  
 XX  
 DE SARS coronavirus right PCR primer, SEQ:573.  
 XX  
 KM Vaccine; nucleic acid vaccine; drug screening; diagnosis;  
 KM SARS coronavirus infection; infection; respiratory disease; virucide;  
 KM PCR; primer; ss.  
 XX

OS SARS coronavirus.  
 XX  
 PN WO2004092360-A2.  
 XX  
 PD 28-OCT-2004.  
 XX  
 PF 09-APR-2004; 2004WO-US011710.  
 XX  
 PR 10-APR-2003; 2003US-0462218P.  
 PR 11-APR-2003; 2003US-0462465P.  
 PR 12-APR-2003; 2003US-0462418P.  
 PR 13-APR-2003; 2003US-0462748P.  
 PR 14-APR-2003; 2003US-0463109P.  
 PR 15-APR-2003; 2003US-0463460P.  
 PR 16-APR-2003; 2003US-0463668P.  
 PR 17-APR-2003; 2003US-0463983P.  
 PR 18-APR-2003; 2003US-0463971P.  
 PR 22-APR-2003; 2003US-0464838P.  
 PR 22-APR-2003; 2003US-0464899P.  
 PR 23-APR-2003; 2003US-0465272P.  
 PR 24-APR-2003; 2003US-0465352P.  
 PR 05-MAY-2003; 2003US-0468312P.  
 PR 22-MAY-2003; 2003US-0473144P.  
 PR 14-AUG-2003; 2003US-0495024P.  
 PR 23-SEP-2003; 2003US-0505652P.  
 PR 11-OCT-2003; 2003US-0510781P.  
 PR 11-DEC-2003; 2003US-0529464P.  
 PR 12-JAN-2004; 2004US-0536177P.  
 PR 07-APR-2004; 2004US-0560757P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;  
 PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JF,  
 PI Klenk HD, Valiante N;  
 XX  
 DR WPI, 2004-766863/75.  
 XX  
 PT Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of  
 PT severe acute respiratory syndrome virus (SARS), useful as vaccine for  
 PT SARS.  
 XX  
 PS Claim 59; SEQ ID NO 573; 839pp; English.  
 XX  
 CC The invention relates to isolated polypeptides of the severe acute  
 CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike  
 CC (S or E2), env (E or SM), membrane (M or E1), hemagglutinin-esterase (HE  
 CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab  
 CC (replicase) polypeptides and their proteolytic fragments. The invention  
 CC also relates to antibodies which recognise the polypeptides; nucleic  
 CC acids encoding the SARS virus polypeptides; primers specific for SARS  
 CC virus nucleic acid sequences; kits for amplifying SARS virus target  
 CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length  
 CC which is able to inactivate the SARS virus in a mammalian cell; an  
 CC expression construct for recombinant expression of a SARS virus spike  
 CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-  
 CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS  
 CC viral antigen. The invention additionally provides a vaccine for the  
 CC treatment or prevention of SARS comprising an inactivated SARS virus, a  
 CC killed SARS virus, an attenuated SARS virus, a split SARS virus  
 CC preparation, or at least one purified SARS virus antigens; methods of  
 CC making inactivated SARS virus and vaccines containing it; an alpha-virus  
 CC replicon particle comprising one or more SARS virus antigens; and a  
 CC vaccine comprising one or more SARS virus antigens and one or more  
 CC respiratory virus antigens. The invention further encompasses a method of  
 CC identifying a therapeutically active agent by measuring the effect of the  
 CC agent on a SARS-related enzyme, and a method of treating a SARS patient  
 CC using small molecule viral inhibitors. The SARS virus polypeptides and  
 CC nucleic acids can be used in the preparation and manufacture of vaccines  
 CC for the treatment or prevention of SARS. The SARS virus polypeptides,  
 CC antibodies against them, and SARS virus-specific primers and kits  
 CC containing them are useful for diagnosing or identifying the presence of  
 CC SARS in a biological sample. The present sequence represents a PCR primer

CC for amplifying a SARS coronavirus gene. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCATGTCAC 12  
 |||||  
 Db 4 CTCATGTCAC 14

RESULT 30  
 ADL96404  
 ID ADL96404 standard; DNA; 14 BP.  
 XX

AC ADL96404;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX

DE Acute myeloid leukaemia (AML) associated EST seqid 303.

XX cytostatic; gene therapy; microarray; gene expression characteristic;  
 KM haematopoietic cell; haematopoiesis; myeloid leukaemia; EST;  
 KM expressed sequence tag; acute myeloid leukaemia; AML; translocation; t(9;  
 KM 11); ss.  
 XX

OS Homo sapiens.  
 XX  
 PN US2003165949-A1.

PD 04-SBP-2003.

XX 23-DEC-2002; 2002US-00329465.

PF 27-DEC-2001; 2001US-0343826P.

XX (WANG/) WANG S M.  
 PA (LEES/) LEE S.  
 PA (CHEN/) CHEN J.  
 PA (ZHOU/) ZHOU G.  
 PA (ROWL/) ROWLEY J D.

XX Wang SM, Lee S, Chen J, Zhou G, Rowley JD;  
 PI WPI; 2003-863699/80.

DR New microarray for measuring gene expression characteristics of  
 XX hematopoietic cells, useful for preparing a composition for diagnosing or  
 PT treating myeloid leukemia.  
 PT

XX Example 3; SEQ ID NO 303; 32bp; English.

XX The invention describes a microarray for measuring gene expression  
 CC characteristics of haematopoietic cells comprising at least 5  
 CC polynucleotides having distinct sequences. Also described are: a method  
 CC of diagnosing or treating an abnormality associated with haematopoiesis;  
 CC and diagnosing myeloid leukemia in a patient. The microarray is useful  
 CC for preparing a composition for diagnosing or treating myeloid leukaemia.  
 CC This sequence represents an expressed sequence tag (EST) isolated from a  
 CC cell of a patient with acute myeloid leukaemia with the t(9;11)  
 CC translocation that results in the mixed-lineage leukaemia (MML)-AF9  
 CC fusion protein.  
 CC

XX Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 54.0%; Score 10.8; DB 1; Length 14;  
 Best Local Similarity 85.7%; Pred. No. 22;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CATGTCACATGGA 17  
 |||||  
 Db 1 CATGTCACAAAGGA 14

RESULT 31  
 AAX31458  
 ID AAX31458 standard; DNA; 15 BP.  
 XX

AC AAX31458;  
 XX

DT 21-MAY-1999 (first entry)  
 XX

DE Tag sequence of a transcript decreased in colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;  
 KM diagnosis; prognosis; treatment; ss.  
 KM

XX Homo sapiens.  
 OS

PN W09853319-A2.

PD 26-NOV-1998.

XX 20-MAY-1998; 98WO-US010277.

PF 21-MAY-1997; 97US-0047352P.

XX (UYUO ) UNIV JOHNS HOPKINS.

PA Vogelstein B, Kinzler KM;  
 PI Vogelstein B, Kinzler KM;  
 PT WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the  
 PT diagnosis, prognosis and treatment of cancers, particularly colon and  
 PT pancreatic cancer.  
 PT

XX Claim 1, Page 51; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are  
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or  
 CC in both. The tag sequences can be used to identify genes by matching the  
 CC tag to a gen data base member, or by using the tag sequences as probes to  
 CC isolate unidentified genes from cDNA libraries. The tag sequences can  
 CC also be used in a method for diagnosing colon or pancreatic cancer in a  
 CC sample suspected of being neoplastic. The method comprises comparing the  
 CC level of at least one transcript in a first sample of a tissue to a  
 CC second sample, where the first sample is a colonic tissue suspected of  
 CC being neoplastic and the second sample is a normal human colonic tissue.  
 CC The transcript is identified by a tag selected from AAX30947-31815. The  
 CC methods of the invention can be used in the diagnosis, prognosis and  
 CC treatment of cancer  
 CC

XX SQ Sequence 15 BP; 3 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 54.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 25;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CATGTCACATGGA 17  
 |||||  
 Db 1 CATGTCACATGGA 14

RESULT 32  
 AAF51885/C  
 ID AAF51885 standard; DNA; 15 BP.  
 XX

AC AAF51885;  
 XX

DT 30-MAR-2001 (first entry)



```
XX
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNITV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 57; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (1)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX Sequence 15 BP; 3 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 54.0%; Score 10.8; DB 1; Length 15;
XX Best Local Similarity 85.7%; Pred. No. 25;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4 CATGTCACATGGA 17
XX 1 CATGCCACATGGA 14
XX
XX Db
XX
XX RESULT 35
XX ADQ82962/c
XX ID ADQ82962 standard; DNA; 14 BP.
XX
XX ADQ82962;
XX
XX 07-OCT-2004 (first entry)
XX
XX Extended hairpin tail primer #22 for SNP detection method.
XX
XX ss; primer; single nucleotide polymorphism; SNP; amplification;
XX hairpin primer; alleles; drug resistance.
XX
XX Mycobacterium tuberculosis.
XX
XX WO2004061134-A1.
XX
XX 22-JUL-2004.
XX
XX 24-DEC-2003; 2003WO-US041136.
XX
XX 27-DEC-2002; 2002US-0437165P.
XX
XX (UYNE-) UNITV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Alland D, Hazdon MH;
XX
XX WPI; 2004-553374/53.
XX
XX Detecting single nucleotide polymorphism (SNP) in an organism, useful for
XX identifying SNPs responsible for drug resistance, comprises amplifying a
XX nucleic acid sequence of an organism using a hairpin shaped primer.
XX
XX Example 1; SEQ ID NO 106; 53pp; English.
XX
XX
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XX
XX The invention relates to a method of detecting a single nucleotide
XX polymorphism (SNP) in an organism by amplifying a nucleic acid sequence
XX of an organism using a hairpin shaped primer that discriminates between
XX different alleles by situating its 3' nucleotide at the location of a
XX SNP, and measuring threshold cycle or amplification efficiency or amount
XX of amplified product. A lower amplification efficiency or delayed
XX threshold cycle or a difference in the amount of amplified product is
XX indicative of a mismatch between the primer and the organism and a SNP in
XX the organism. The method is useful for efficiently identifying SNPs
XX responsible for drug resistance of infective organisms. The method and
XX kit are useful for analysing large number of isolates, thus providing a
XX means for comprehensive understanding of the frequency and position of
XX mutations in an organism. This sequence corresponds to an extended
XX hairpin tail primer used in the method of the invention
XX
XX Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 52.0%; Score 10.4; DB 1; Length 14;
XX Best Local Similarity 91.7%; Pred. No. 25;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 TGGTCACATGGA 17
XX 12 TGGTCACATGGA 1
XX
XX Db
XX
XX RESULT 36
XX ADQ82964/c
XX ID ADQ82964 standard; DNA; 14 BP.
XX
XX ADQ82964;
XX
XX 07-OCT-2004 (first entry)
XX
XX Extended hairpin tail primer #24 for SNP detection method.
XX
XX ss; primer; single nucleotide polymorphism; SNP; amplification;
XX hairpin primer; alleles; drug resistance.
XX
XX Mycobacterium tuberculosis.
XX
XX WO2004061134-A1.
XX
XX 22-JUL-2004.
XX
XX 24-DEC-2003; 2003WO-US041136.
XX
XX 27-DEC-2002; 2002US-0437165P.
XX
XX (UYNE-) UNITV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Alland D, Hazdon MH;
XX
XX WPI; 2004-553374/53.
XX
XX Detecting single nucleotide polymorphism (SNP) in an organism, useful for
XX identifying SNPs responsible for drug resistance, comprises amplifying a
XX nucleic acid sequence of an organism using a hairpin shaped primer.
XX
XX Example 1; SEQ ID NO 108; 53pp; English.
XX
XX The invention relates to a method of detecting a single nucleotide
XX polymorphism (SNP) in an organism by amplifying a nucleic acid sequence
XX of an organism using a hairpin shaped primer that discriminates between
XX different alleles by situating its 3' nucleotide at the location of a
XX SNP, and measuring threshold cycle or amplification efficiency or amount
XX of amplified product. A lower amplification efficiency or delayed
XX threshold cycle or a difference in the amount of amplified product is
XX indicative of a mismatch between the primer and the organism and a SNP in
XX the organism. The method is useful for efficiently identifying SNPs
XX responsible for drug resistance of infective organisms. The method and
XX kit are useful for analysing large number of isolates, thus providing a
XX
```

CC means for comprehensive understanding of the frequency and position of  
 CC mutations in an organism. This sequence corresponds to an extended  
 CC hairpin tail primer used in the method of the invention  
 XX  
 SQ Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 25;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 TGGTCACATGGA 17  
 |||||  
 Db 12 TGGTCACATGCA 1

RESULT 37  
 AAT36745/c  
 ID AAT36745 standard; DNA; 14 BP.

XX  
 AC AAT36745;  
 XX  
 DT 22-APR-1997 (first entry)  
 XX

DE Antisense oligonucleotide to cdk4 gene.

KM Antisense; phosphorylation; retinoblastoma; tumour suppressor; ribozyme;  
 KW antagonist; kinase; cyclin; cdk4; Rb; ss.

XX Synthetic.

XX DE19539130-A1.

XX PD 29-AUG-1996.

XX PF 20-OCT-1995; 95DE-01039130.

XX PR 28-FEB-1995; 95DE-01008734.

XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX PI Straus M, Bartek J, Lukas J, Sandig V;

XX DR WPI; 1996-394264/40.

PT Compens. for treating tumour or other hyperplasias - contg. co-operative  
 PT gene, antisense or ribozyme against kinase or cyclin or other inhibitor  
 of Rb phosphorylation.  
 XX

PS Claim 12; Page 4; 7pp; German.

XX The oligonucleotides AAT36744-50 represent antisense oligonucleotides  
 CC targeted to genes encoding proteins that interact with, pref. by  
 CC phosphorylating the retinoblastoma (Rb) protein. The oligonucleotides are  
 CC used in a novel method of treating tumours by using: (a) tumour  
 CC suppressor genes that co-operate with the Rb suppressor, (b) antisense or  
 CC ribozymes that are antagonistic to kinases or cyclins, or (c) other  
 CC compounds that inhibit Rb phosphorylation. This oligonucleotide is  
 CC directed to the cyclin-dependent kinase cdk4 gene  
 XX  
 SQ Sequence 14 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GGTACATGG 16  
 |||||  
 Db 14 GTTCACATGG 5

RESULT 38  
 AAH89017/c  
 ID AAH89017 standard; DNA; 14 BP.

XX  
 AC AAH89017;  
 XX  
 DT 09-SEP-2004 (revised)  
 DT 27-FEB-2002 (first entry)  
 XX

DE Human polymorphic oligonucleotide U54701 fragment #18.

KW Human; single nucleotide polymorphic; SNP; forensic science;  
 KW paternity testing; phenotypic trait; genetic mapping; animal breeding;  
 KW plant breeding; ds.  
 XX

OS Homo sapiens.  
 OS Unidentified.

EH Key Location/Qualifiers  
 FT variation 11  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"

XX WO200134840-A2.

XX PD 17-MAY-2001.

XX PF 10-NOV-2000; 2000WO-US030766.

XX PR 10-NOV-1999; 99US-0164596P.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Au K, Chen J, Patil N, Thomas D;

XX DR WPI; 2001-335945/35.

XX New polymorphic sites derived from the human genome are useful to  
 PT determine sites correlating with phenotypic traits, particularly disease,  
 PT and also in forensics and paternity testing.  
 XX

PS Claim 69; Page 11; 43pp; English.

XX The present invention relates to human oligonucleotides comprising a  
 CC single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present  
 CC sequence is one such oligonucleotide. The oligonucleotides can be used in  
 CC forensics, paternity testing, correlation of polymorphisms with  
 CC phenotypic traits, genetic mapping of phenotypic traits and marker  
 CC assisted breeding of animals and crop plants  
 CC

CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key

XX SQ Sequence 14 BP; 2 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTTCACATGGA 17  
 |||||  
 Db 10 GTTCACATGGA 1

RESULT 39  
 ABH45285/c  
 ID ABH45285 standard; DNA; 13 BP.

XX ABH45285;  
 AC  
 XX  
 DT 22-FEB-2002 (first entry)  
 DT  
 XX

DE Oligonucleotide SEQ ID NO 245262 for detecting SNP TSC0059887.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 245262; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 49.0%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 27;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 6 TGGTCACATGGAT 18  
Db |||||  
1 TGGTAACGTGGAT 1  
XX  
RESULT 40  
ABH45284  
ID ABH45284 standard; DNA; 13 BP.  
XX  
AC ABH45284;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 245261 for detecting SNP TSC0059897.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA

XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 245261; 29pp + Sequence Listing; German.  
PS  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 49.0%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 27;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 6 TGGTCACATGGAT 18  
Db |||||  
1 TGGTAACGTGGAT 13  
XX  
RESULT 41  
ABH28185/c  
ID ABH28185 standard; DNA; 13 BP.  
XX  
AC ABH28185;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 228162 for detecting SNP TSC0055641.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 228162; 29pp + Sequence Listing; German.  
PS  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)



DT	16-JUN-2005	(first entry)
XX		
DE	Human SNP detection related oligonucleotide #1689.	
XX		
KM	ss, haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;	
KM	immune disorder; cardiovascular disease; metabolic disorder;	
KM	respiratory disease; musculoskeletal disease; renal disease;	
XX	nephrotropic; endocrine disease; genitourinary disease.	
OS	Homo sapiens.	
XX		
PM	WO2005030952-A1.	
XX		
PD	07-APR-2005.	
XX		
PF	30-SEP-2004; 2004WO-JP014784.	
XX		
PR	30-SEP-2003; 2003JP-00342519.	
XX	28-MAY-2004; 2004JP-00158717.	
PA	(RIKE ) RIKEN KK.	
PA	(STAG-) STAGEN CO LTD.	
PA	(SEKI/) SEKINE A.	
PA	(IIDA/) IIDA A.	
PA	(SAIT/) SAITO S.	
PI	Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;	
XX		
DR	WPI; 2005-305936/31.	
XX		
PT	Analyzing haplotype, by detecting polymorphism in drug-related genes,	
PT	electing common polymorphism (CP), building haplotype block using CP,	
PT	specifying CP within block, specifying tag polymorphism from CP within	
XX	block.	
PS	Disclosure; SEQ ID NO 1689; 1290bp; Japanese.	
XX		
CC	The invention relates to a method of analyzing haplotype, by detecting	
CC	gene polymorphism in drug-related genes such as aryl acetylarnide	
CC	deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,	
CC	sub-family A (ABCI), member 1. The method is useful for analyzing	
CC	haplotype. The method is useful for estimating the sensitivity or disease	
CC	of a medicine or a foreign material, for selecting medicine for	
CC	preventing or treating diseases, for determining appropriate dosage of	
CC	interaction for preventing or treating a disease, for analyzing a drug	
CC	sensitivity, and for determining the related polymorphism relative to the	
CC	sensitivity of the medicine, foreign material or disease. The diseases	
CC	include malignant tumor, immune disorder circulatory disease, metabolic	
CC	disease, kidney disease, respiratory disease and muscle associated	
CC	disease. The method enables analysis of the individual differences	
CC	related to the sensitivity of a medicine, using a haplotype, without	
CC	using each single nucleotide polymorphism. The present sequence	
CC	represents a human SNP detection related oligonucleotide.	
XX		
SO	Sequence 13 BP; 2 A; 5 C; 3 G; 3 T; 0 U; 0 Other;	
XX		
QY	Query Match	47.0%; Score 9.4; DB 1; Length 13;
XX	Best Local Similarity	90.9%; Pred. No. 31;
XX	Matches 10; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
DB	1 CCTCATGATCA 11	
	2 CCTCATGCTCA 12	
XX		
RESULT 46		
ID	AED86939	
XX	AED86939 standard; DNA; 13 BP.	
XX	AED86939;	
DT	12-JAN-2006	(first entry)
XX		

```

DE Polyamide-binding target oligonucleotide I, SEQ ID NO:12.
XX
XX Gene expression; transcription factor inhibitor; DNA footprinting; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_binding 1..13
FT /*tag= a
FT /bound_moiety= "Bases 13-1 of SEQ ID NO:13"
FT 7..10
FT /*tag= b
FT /bound_moiety= "Imidazole- and pyrrole-containing
FT polyamide chain"
FT /note= "Polyamide chain binds to the minor groove of the
FT dsdNA in a sequence-specific manner"
XX
XX
XX US6958240-B1.
XX
XX 25-OCT-2005.
XX
XX 12-AUG-1999; 99US-00374704.
XX
XX 26-FEB-1996; 96US-00607078.
XX 20-FEB-1997; 97MO-US003332.
XX 08-APR-1997; 97US-0043444P.
XX 16-APR-1997; 97US-0042022P.
XX 21-APR-1997; 97US-00837524.
XX 08-MAY-1997; 97US-00853522.
XX
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Baird EE, Deryan PB;
XX
XX WPI; 2005-807194/82.
XX
XX Novel polyamides comprising amino acids having N-methylpyrrole, 3-hydroxy
XX N-methylpyrrole and/or N-methylimidazole groups and positive patches
XX having rigid groups adjacent to positively charged groups, useful for
XX inhibiting gene expression.
XX
XX
XX Example 4; SEQ ID NO 12; 43bp; English.
XX
XX The invention relates to a polyamide molecule which specifically binds to
XX a predetermined site in the minor groove of a double-stranded DNA
XX molecule in a sequence-specific manner and which contains an alpha-amino
XX acid domain (termed the "positive patch") which contacts nucleotides in
XX the major groove and thus inhibits the activity of major groove DNA-
XX binding proteins. The polyamide molecule comprises one or more amino
XX acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-
XX methylimidazole group, where one or more of these amino acid(s) are not
XX alpha-amino acids, and a positive patch consisting of a 2 amino acid
XX rigid group adjacent to a positively charged group (such as a positively
XX charged amino acid). The polyamides of the invention inhibit gene
XX expression by displacing or preventing the function of DNA-binding
XX proteins such as transcription factors. The invention also relates to a
XX method of inhibiting gene expression by contacting a regulatory sequence
XX of a gene with a polyamide of the invention. The polyamide of the
XX invention is useful for inhibiting the binding and activity of DNA-
XX binding proteins, thus inhibiting gene expression. Sequences AED6939-
XX AED6940 represent the two strands of a double-stranded oligonucleotide
XX which is capable of being bound by a polyamide of the invention. This
XX oligonucleotide was used in DNase I footprinting in an example of the
XX invention to determine the optimum positive patch peptide sequence for
XX inhibition of protein binding.
XX
XX Sequence 13 BP; 5 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. NO. 31;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 3 TCATGTCACA 13

```

```

DB
XX |||||
XX 3 TCATGTCACA 13
XX
XX RESULT 47
XX AED6940/c
XX ID AED6940 strand; DNA; 13 BP.
XX
XX AED6940;
XX
XX 12-JAN-2006 (first entry)
XX
XX Polyamide-binding target oligonucleotide I, SEQ ID NO:13.
XX
XX Gene expression; transcription factor inhibitor; DNA footprinting; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_binding 1..13
FT /*tag= a
FT /bound_moiety= "Bases 13-1 of SEQ ID NO:12"
FT 4..13
FT misc_binding 4..13
FT /*tag= d
FT /bound_moiety= "Imidazole- and pyrrole-containing
FT polyamide chain with Arg-Pro-Arg-Arg-Arg positive
FT patch"
FT /note= "Polyamide chain binds to the minor groove of the
FT dsdNA in a sequence-specific manner"
FT 4..10
FT misc_binding 4..10
FT /*tag= c
FT /bound_moiety= "Imidazole- and pyrrole-containing
FT polyamide chain with Arg-Pro-Arg positive patch"
FT /note= "Polyamide chain binds to the minor groove of the
FT dsdNA in a sequence-specific manner"
XX
XX
XX Example 4; SEQ ID NO 13; 43bp; English.
XX
XX The invention relates to a polyamide molecule which specifically binds to
XX a predetermined site in the minor groove of a double-stranded DNA
XX molecule in a sequence-specific manner and which contains an alpha-amino
XX acid domain (termed the "positive patch") which contacts nucleotides in
XX the major groove and thus inhibits the activity of major groove DNA-
XX binding proteins. The polyamide molecule comprises one or more amino
XX acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-
XX methylimidazole group, where one or more of these amino acid(s) are not
XX alpha-amino acids, and a positive patch consisting of a 2 amino acid
XX rigid group adjacent to a positively charged group (such as a positively
XX charged amino acid). The polyamides of the invention inhibit gene
XX expression by displacing or preventing the function of DNA-binding
XX proteins such as transcription factors. The invention also relates to a
XX method of inhibiting gene expression by contacting a regulatory sequence
XX of a gene with a polyamide of the invention. The polyamide of the
XX invention is useful for inhibiting the binding and activity of DNA-
XX binding proteins, thus inhibiting gene expression. Sequences AED6939-
XX AED6940 represent the two strands of a double-stranded oligonucleotide
XX which is capable of being bound by a polyamide of the invention. This
XX oligonucleotide was used in DNase I footprinting in an example of the
XX invention to determine the optimum positive patch peptide sequence for
XX inhibition of protein binding.
XX
XX Sequence 13 BP; 5 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. NO. 31;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 3 TCATGTCACA 13

```

CC binding proteins. The polyamide molecule comprises one or more amino  
CC acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-  
CC methylindazole group, where one or more of these amino acid(s) are not  
CC alpha-amino acids, and a positive patch consisting of a 2 amino acid  
CC rigid group adjacent to a positively charged group (such as a positively  
CC charged amino acid). The polyamides of the invention inhibit gene  
CC expression by displacing or preventing the function of DNA-binding  
CC proteins such as transcription factors. The invention also relates to a  
CC method of inhibiting gene expression by contacting a regulatory sequence  
CC of a gene with a polyamide of the invention. The polyamide of the  
CC invention is useful for inhibiting the binding and activity of DNA-  
CC binding proteins, thus inhibiting gene expression. Sequences AED6939-  
CC AED6940 represent the two strands of a double-stranded oligonucleotide  
CC which is capable of being bound by a polyamide of the invention. This  
CC oligonucleotide was used in DNase I footprinting in an example of the  
CC invention to determine the optimum positive patch peptide sequence for  
CC inhibition of protein binding.

XX SQ Sequence 13 BP; 4 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 31;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGGTCA 13  
|||||||  
Db 11 TCATGGTCA 1

RESULT 48  
AAQ8597/c:  
ID AAQ8597 standard; DNA; 12 BP.

XX AC AAQ8597;  
XX DT 21-DEC-1995 (first entry)  
XX XX Human mitochondrial D-loop region DNA probe 6-10.

XX DE Tilling strategy; immobilised nucleic acid probe array; mitochondrial DNA;  
XX KM D-loop region; biological chip; hybridisation fingerprint;  
XX KW interrogation position; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
XX FT modified\_base 12  
XX FT /tag= a  
XX FT /note= "3'-end of probe is covalently attached to chip  
XX FT surface"

XX PN WO9511995-A1.

XX PD 04-MAY-1995.

XX PF 26-OCT-1994; 94WO-US012305.

XX PR 26-OCT-1993; 93US-00143312.

XX PA 02-AUG-1994; 94US-00284064.

XX PA (AFPM-) AFFYMAX TECHNOLOGIES NV.

XX PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA,  
XX PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL,  
XX DR WPI; 1995-178867/23.

XX PT New arrays of oligo:nucleotide probes - used for comparing known  
XX PT sequences with variants for detection of mutation(s) and sequencing.  
XX PS Disclosure; Page 108; 223pp; English.

XX CC A DNA chip was prepared for analysing sequences contained in a 1.3kb

CC fragment of human mitochondrial DNA from the D-loop region, the most  
CC polymorphic region of human mitochondrial DNA. The chip comprised a set  
CC of 268 overlapping oligonucleotide probes (see AAQ8421-Q8464) of  
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm  
CC x 1cm array. Each position in the sequence was represented by at least  
CC one probe (usually 2 or more). DNA was amplified from six human donors  
CC and then transcribed to give the 1.3kb RNA transcripts which were  
CC fragmented and hybridised to the chip. For each individual, a unique  
CC hybridisation fingerprint was produced on the chip; all differences could  
CC be correlated with differences in the cloned genomic DNA sequence

XX SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CATGGATGA 20  
|||||||  
Db 11 CATGGATGA 3

RESULT 49  
AAV32269  
ID AAV32269 standard; DNA; 12 BP.

XX AC AAV32269;  
XX XX

XX DT 18-AUG-1998 (first entry)  
XX XX

XX DE Random primed reverse transcription PCR primer 114.

XX KW RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;  
XX KM differential gene expression; ss.

XX OS Synthetic.

XX PN WO9813521-A1.

XX PD 02-APR-1998.

XX PF 26-SEP-1997; 97WO-BP005290.

XX PR 27-SEP-1996; 96GB-00020216.

XX PA (SANR-) FOND CENT SAN RAFFAELLE DEL MONTE TABOR.

XX PI Consalez G, Fesce R;  
XX PI

XX DR WPI; 1998-230725/20.

XX PT Differential screening of gene expression by reverse transcription  
XX PT polymerase chain reaction - uses random priming with primers selected for  
XX PT high efficiency and selectivity by computer screening of database(s).

XX PS Claim 9; Page 24; 37pp; English.

XX CC The invention provides a method for the differential screening of gene  
XX CC expression by random primed reverse transcription PCR (RT-PCR). The  
XX CC primer sequences are generated by stimulating PCR reactions on non-  
XX CC redundant mammalian nucleotide sequence databank entries containing at  
XX CC least 1,000 bp of coding region. The primers selected, such as the  
XX CC present one, had to meet various criteria such as having an efficiency  
XX CC index between 2-10, having a selectivity index higher than 1, being 12 bp  
XX CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others  
XX CC in at least 5 of the 8 bases at the 3'-end. The invention claims the  
XX CC selected primers make it possible to use internally primed, PCR-based RNA  
XX CC fingerprinting for simple, exhaustive and systematic analysis of  
XX CC differential gene expression as an advantageous alternative to  
XX CC differential display. The method can also be useful for isolating new  
XX CC coding sequences and to compare known and new genes  
XX SQ Sequence 12 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 1 Other;



KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPICENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 308269; 29pp + Sequence listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. The  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 44.0%; Score 8.8; DB 1; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 33;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CCTCATGTCAC 12  
 DB 1 CCTCATGTCAC 12  
 XX  
 RESULT 53  
 ADM1578  
 ID ADM1578 standard; RNA; 12 BP.  
 XX  
 AC ADM1578;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE siRNA production-related p4 box RNA SeqID15.  
 XX  
 KW short interfering RNA; siRNA; RNA interference; ribozyme; ss.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..4  
 FT misc\_binding /tag= b  
 FT /bound\_moiety= "Itself"  
 FT /note= "Binds nucleotides 12-9 of itself"  
 FT 9..12  
 FT misc\_binding /tag= b  
 FT /bound\_moiety= "Itself"

FT /note= "Binds nucleotides 4-1 of itself"  
 XX  
 XX  
 PN WO2005001039-A2.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PP 28-MAY-2004; 2004WO-US017034.  
 XX  
 PR 29-MAY-2003; 2003US-0474001P.  
 XX  
 PA (UYCR-) UNIV CREIGHTON.  
 XX  
 PI Soukup GA, Kertsburg A;  
 XX  
 DR WPI; 2005-075534/08.  
 XX  
 PT Producing a small, interfering RNA (siRNA) by providing a first or second  
 PT RNA construct comprising a first or second ribozyme operably linked to a  
 PT sense or an antisense strand, respectively of an siRNA.  
 XX  
 PS Example 1; SEQ ID NO 15; 43pp; English.  
 XX  
 CC This invention relates to a novel method of producing a small interfering  
 CC RNA (siRNA). The method comprises providing a first RNA construct  
 CC comprising a first ribozyme operably linked to a sense and antisense  
 CC strand of an siRNA and placing the first and second RNA constructs under  
 CC conditions where the first and second ribozyme catalyze the cleavage of  
 CC the sense and antisense strands of the siRNA from the first and second  
 CC RNA constructs. The present sequence is that of a p4 box RNA which was  
 CC used during the exemplification of the method of the invention.  
 XX  
 SQ Sequence 12 BP; 5 A; 2 C; 3 G; 0 T; 2 U; 0 Other;  
 XX  
 Query Match 44.0%; Score 8.8; DB 1; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 33;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 CATGTCACATG 15  
 DB 1 CAUGGAAACAU 12  
 XX  
 RESULT 54  
 AAQ24034  
 ID AAQ24034 standard; DNA; 12 BP.  
 XX  
 AC AAQ24034;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-SEP-1992 (first entry)  
 XX  
 DE Herpesvirus inhibiting antisense oligonucleotide.  
 XX  
 KW HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;  
 KW Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9205284-A.  
 XX  
 PD 02-APR-1992.  
 XX  
 PF 18-SEP-1991; 91WO-US006646.  
 XX  
 PR 21-SEP-1990; 90US-00586185.  
 XX  
 PA (UYMA-) UNIV MARYLAND BALTIMORE.  
 PA (UYUO) UNIV JOHNS HOPKINS.  
 XX  
 PI Aurelian L, Tso P;  
 XX  
 DR WPI; 1992-132145/16.  
 XX

PT New anti:sense oligo:nucleotide(s) for inhibiting HSV - also used for  
PT diagnosis and for inhibiting HIV activation by herpes virus.  
XX  
PS Claim 1; Page 38; 77pp; English.  
XX  
CC The sequence is that of an antisense oligonucleotide which can be used  
CC for inhibiting growth or replication of herpesviruses. It corresponds to  
CC an antisense sequence of a herpesvirus site, pref. in a gene that is  
CC essential for synthesising nucleic acids e.g. the immediate early genes  
CC or Vmw65. It can be prepd. by solid phase triester or phosphor- amidite  
CC chemistry or by recombinant DNA techniques. It can be used for treating  
CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2  
CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus  
CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the  
CC inhibition of herpesvirus growth or replication may indirectly forestall  
CC the progression of events from HIV exposure to the clinical manifestation  
CC of AIDS. It may also be useful in the detection, diagnosis and  
CC manipulation of herpes virus. See also AAQ3764-Q23788 and AAQ24014-  
CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 12 BP; 5 A; 3 C; 2 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 4 CATGCTACA 13  
|||||  
DB 2 CATGTTACA 11  
|||||  
XX  
RESULT 55  
AAQ30497/C  
ID AAQ30497 standard; DNA; 12 BP.  
XX  
XX AAQ30497;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT 19-MAR-1993 (first entry)  
XX  
XX Adenovirus major late transcription factor element under control of TCER.  
DE  
XX  
XX Transcriptional control recognition element; decoy; cellular RNA;  
KW promoter; hormone receptor element; viral; liver; tissue; viral;  
KM proliferation; linker; NP-1; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX WO9218522-A1.  
PN  
XX  
XX 29-OCT-1992.  
PD  
XX  
XX 17-APR-1992; 92WO-US003205.  
PF  
XX  
XX 18-APR-1991; 91US-00687337.  
PR  
XX  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
PA  
XX  
XX Chu BC, Orgel L;  
PI  
XX  
XX WPI; 1992-382035/46.  
DR  
XX  
XX New oligo-nucleotide(s) config. transcription control recognition element  
PT - stabilised by covalent bonding of two DNA strands, act as decoys for  
PT regulatory protein to modulate specific RNA.  
XX  
XX Disclosure; Page 6; 41pp; English.  
PS  
XX  
XX Transcriptional control recognition element recognition sequences may be  
CC recognised by control proteins and are involved in either enhancing or  
CC repressing transcription of associated sequences. TCR sequences include  
CC promoter elements, hormone receptor elements, viral, cellular, liver or  
CC tissue elements, etc. The sequence represents an exemplary viral and

CC cellular element, the adenovirus major late transcription factor. A  
CC typical application of the TCER recognising oligonucleotides is  
CC inhibition of viral proliferation. See also AAQ30472-518. (Updated on 25-  
CC MAR-2003 to correct PN field.)  
XX  
SQ Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;  
XX  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 7 GGTCACATGG 16  
|||||  
DB 12 GGTCACGTGG 3  
|||||  
XX  
RESULT 56  
AAQ52946/C  
ID AAQ52946 standard; RNA; 12 BP.  
XX  
XX AAQ52946;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT 26-MAY-1994 (first entry)  
XX  
XX Herpes simplex virus target sequence 24.  
DE  
XX  
XX RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; hnRNA;  
KW picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;  
KW papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;  
KW T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;  
KW influenza virus; HSV; herpes simplex virus; vector; immune response;  
KW antibody; ribozyme; viral RNA; treatment; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX WO9232569-A1.  
PN  
XX  
XX 25-NOV-1993.  
PD  
XX  
XX 29-APR-1993; 93WO-US004020.  
PF  
XX  
XX 11-MAY-1992; 92US-00882689.  
PR 14-MAY-1992; 92US-00882712.  
PR 14-MAY-1992; 92US-00882713.  
PR 14-MAY-1992; 92US-00882714.  
PR 14-MAY-1992; 92US-00882823.  
PR 14-MAY-1992; 92US-00882824.  
PR 14-MAY-1992; 92US-00882866.  
PR 14-MAY-1992; 92US-00882868.  
PR 14-MAY-1992; 92US-00882889.  
PR 14-MAY-1992; 92US-00882921.  
PR 14-MAY-1992; 92US-00882922.  
PR 14-MAY-1992; 92US-00883823.  
PR 14-MAY-1992; 92US-00883849.  
PR 14-MAY-1992; 92US-00884073.  
PR 14-MAY-1992; 92US-00884074.  
PR 14-MAY-1992; 92US-00884333.  
PR 14-MAY-1992; 92US-00884422.  
PR 14-MAY-1992; 92US-00884431.  
PR 14-MAY-1992; 92US-00884436.  
PR 14-MAY-1992; 92US-00923738.  
PR 31-JUL-1992; 92US-00923738.  
PR 26-AUG-1992; 92US-00935854.  
PR 26-AUG-1992; 92US-00935854.  
PR 18-SEP-1992; 92US-00948359.  
PR 15-OCT-1992; 92US-00963322.  
PR 07-DEC-1992; 92US-00967129.  
PR 07-DEC-1992; 92US-00967130.  
PR 07-DEC-1992; 92US-00967133.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX

PI Draper KG, Dudycz LM, Mcswigen JA, Macejak DG, Holeczek JJ;  
PI Mamone JA;  
XX WPI; 1993-386599/48.  
XX Enzymatic RNA molecules - used to inhibit viral replication, infection  
PT and gene expression.  
XX  
PS Claim 5; Fig 15; 287pp; English.  
XX  
CC The sequences (AA052923-Q53037) are pref. herpes simplex virus target  
CC complements for enzymatic RNA molecules. The RNA molecules are  
CC complementary to a substrate binding region in the specified gene target.  
CC They also have enzymatic activity, in that they specifically cleave RNA  
CC in the target. The ERNs interfere with viral replication and therefore  
CC have anti-viral properties. They can be used to attenuate viruses to be  
CC used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated  
CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct  
CC PI field.)  
XX  
SQ Sequence 12 BP; 2 A; 4 C; 4 G; 0 T; 2 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 TCATGCTCAC 12  
Db 12 TCATGGCCAC 3  
RESULT 57  
AAZ59958/C  
ID AAZ59958 standard; DNA; 12 BP.  
XX  
XX AAZ59958;  
AC  
XX  
DT 19-APR-2000 (first entry)  
XX  
DE Adenovirus Ad5 major late promoter (MLP) upstream promoter element (UPB).  
XX  
XX Major late promoter; MLP; mutation; upstream promoter element; UPB;  
KM recombinant adenovirus; B1 region deficiency; gene therapy;  
KM replication incompetent; ds.  
XX  
OS Mastadenovirus.  
XX  
XX WO200000628-A1.  
PN  
XX  
PD 06-JAN-2000.  
XX  
PP 24-JUN-1999; 99WO-US014333.  
XX  
PR 26-JUN-1998; 98US-00105515.  
XX  
XX  
PA (GENV-) GENVEC INC.  
XX  
PI Brough DE, Kovesdi I;  
XX  
DR WPI; 2000-147271/13.  
XX  
PT Novel replication-defective adenoviruses with a mutated major late  
PT promoter used to study viral molecular genetics and as viral vectors for  
PT genetic transfer.  
PS  
XX Disclosure; Page 18; 23pp; English.  
XX  
CC The invention relates to a recombinant adenovirus comprising a genome  
CC with a deficiency in the B1 region and a mutation in the major late  
CC promoter (MLP), so that the MLP is less active within a cell other than a  
CC packaging cell. The recombinant adenoviruses are highly useful in  
CC biological research. They can be used to study viral molecular genetics  
CC and cytotoxicity, and to investigate the cell biology of viral growth and

CC infection. They can also be used to investigate molecular and cellular  
CC biology of gene expression and regulation in novel genetic backgrounds,  
CC e.g., interaction of gene products, ability of transcription factors to  
CC transregulate gene expression via promoter, or enhancer elements  
CC engineered into the adenovirus. The adenoviruses are also useful as gene  
CC transfer vehicles, e.g., to introduce transgenes into tissues or cells,  
CC and may thus be used as gene therapy vectors. The recombinant  
CC adenoviruses can be grown without the presence of DNA complementary to  
CC the wild type adenoviral MLP, substantially reducing the probability for  
CC generating replication competent adenoviruses (RCA). In addition, because  
CC the viruses have a MLP which greatly attenuates 11-15 gene expression in  
CC nonpermissive host cells, they are less able than first generation  
CC vectors to express late viral gene products in a host cell. Sequences  
CC AAZ59957-Z59960 represent promoter elements of the MLP of adenovirus  
CC serotype 5 (Ad5). The present sequence represents the upstream promoter  
CC element (UPB), which is located 63 bp upstream of the transcriptional  
CC start site  
XX  
SQ Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GGTCAATGG 16  
Db 12 GGTCACTGG 3  
RESULT 58  
AAA30866  
ID AAA30866 standard; DNA; 12 BP.  
XX  
XX AAA30866;  
AC  
XX  
DT 19-SEP-2000 (first entry)  
XX  
DE Fragment of a plasmid for expressing a ubiquitin monomer.  
XX  
XX Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;  
KM plasmid fragment; ss.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200036129-A1.  
PN  
XX  
PD 22-JUN-2000.  
XX  
PP 11-DEC-1998; 98WO-SG000103.  
XX  
XX  
PR 11-DEC-1998; 98WO-SG000103.  
XX  
XX  
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.  
XX  
PI Fang R, Wu J, Chen X;  
XX  
XX  
DR WPI; 2000-431604/37.  
XX  
PT Production of desired protein in plants or plant cells by linking a  
PT ubiquitin monomer coding sequence upstream of the gene encoding the  
PT desired protein.  
PS  
XX Example 2; Page 20; 42pp; English.  
XX  
CC This sequence represents a fragment of a plasmid expressing a fusion  
CC construct encoding a fusion protein having a ubiquitin monomer linked to  
CC a protein of interest. The invention relates to a method for enhancing  
CC production of a desired protein in a plant or plant cell by inserting a  
CC nucleic acid (NA) encoding a ubiquitin monomer upstream of a NA encoding  
CC the desired protein, where the fusion construct encodes a fusion protein  
CC and expression is not controlled by the ubiquitin promoter. The invention  
CC also relates to a NA acid vector a NA vector able to transform a plant  
CC cell, that comprises NA encoding a fusion protein having a ubiquitin



KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIC-) EPIDENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS  
 PS Claim 1; SEQ ID NO 372362; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 42.0%; Score 8.4; DB 1; Length 12;  
 XX Best Local Similarity 90.0%; Pred. No. 37;  
 XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 11 ACATGATGA 20  
 XX | |||||  
 DB 2 ATATGATGA 11  
 XX  
 XX  
 XX RESULT 62  
 XX ABH84083/C  
 XX ID ABH84083 standard; DNA; 12 BP.  
 XX  
 XX ABH84083;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX  
 XX Oligonucleotide primer SEQ ID NO 284076 for detecting SNP TSC0011646.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX Claim 1; SEQ ID NO 304734; 29pp + Sequence Listing; German.

XX  
 XX (EPIC-) EPIDENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS  
 PS Claim 1; SEQ ID NO 284076; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 42.0%; Score 8.4; DB 1; Length 12;  
 XX Best Local Similarity 90.0%; Pred. No. 37;  
 XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 11 ACATGATGA 20  
 XX | |||||  
 DB 11 ATATGATGA 2  
 XX  
 XX  
 XX RESULT 63  
 XX AB104761  
 XX ID AB104761 standard; DNA; 12 BP.  
 XX  
 XX AB104761;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX  
 XX Oligonucleotide primer SEQ ID NO 304734 for detecting SNP TSC0021079.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIC-) EPIDENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS  
 PS Claim 1; SEQ ID NO 304734; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

CC Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

QY Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ACATGATGCA 20  
Db 2 ACGTGGATGA 11

#### RESULT 64

ABH67680  
ID ABH67680 strand; DNA; 12 BP.

AC ABH67680;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267657 for detecting SNP TSC0000420.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single-nucleotide polymorphisms and cytosine  
methylation status.

PS Claim 1; SEQ ID NO 267657; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SEQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

QY Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ACATGATGCA 20  
Db 1 ATATGATGCA 10

#### RESULT 65

ABH08303/C  
ID ABH08303 strand; DNA; 12 BP.

AC ABH08303;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 308276 for detecting SNP TSC0022938.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single-nucleotide polymorphisms and cytosine  
methylation status.

PS Claim 1; SEQ ID NO 308276; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SEQ Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

QY Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ACATGATGCA 20  
Db 12 ACGTGGATGA 3

#### RESULT 66

ABH29750/C

ID AB129750 standard; DNA; 12 BP.  
XX  
AC AB129750;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 329723 for detecting SNP TSC003511.  
XX  
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN MO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001MO-IB000713.  
XX  
PR 07-APR-2000; 2000DB-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 329723; 29bp + Sequence listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and AB100010-AB12073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pat\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
XX Best Local Similarity 90.0%; Pred. No. 37;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 11 ACATGATGA 20  
XX | |||||  
XX 11 AATGATGA 2  
XX  
Db 11 AATGATGA 2  
XX  
RESULT 67  
AAH49257  
ID AAH49257 standard; DNA; 12 BP.  
XX  
AC AAH49257;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE PNA-forming oligonucleotide #20.  
XX  
KM Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
KM antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;  
KM integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;  
KM peptide nucleic acid; ss.  
XX

OS Synthetic.  
XX  
PN EP1113021-A2.  
XX  
PD 04-JUL-2001.  
XX  
PF 08-MAR-1995; 2001EP-00104012.  
XX  
PR 14-MAR-1994; 94DB-04408528.  
PR 08-MAR-1995; 95EP-00103332.  
XX  
XX (AVER ) AVENTIS PHARMA DEUT GMBH.  
XX  
PI Uhlmann B, Breipohl G;  
PI WPI; 2001-591267/67.  
XX  
DR New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
XX PT for treating e.g. cancer, also as diagnostic probes and primers.  
XX  
PS Example 43; Page 46; 54pp; German.  
XX  
CC This invention describes novel polyamide-oligonucleotide derivatives (I)  
XX CC and their physiologically acceptable salts of formula F(DNA-Li)q(PNA-  
XX CC Li)r(DNA-Li)s(PNA)t'XF' where q, r, s, t = 0 or 1, with the sum of  
XX CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid  
XX CC (such as DNA or RNA or their known derivatives); Li = covalent linkage  
XX CC between DNA and PNA, i.e. a bond or a residue containing at least one  
XX CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure  
XX CC containing at least one nucleobase different from thymine; and F, F' =  
XX CC end groups and/or are connected through a covalent bond. The products of  
XX CC the invention have anticancer, antiproliferative, antiviral, hepatotropic  
XX CC and vasotropic activity and can be used for the inhibition of gene  
XX CC expression by antisense, ribozyme, sense, or triple-helix methods, or by  
XX CC binding to proteins (aptamers). (I) are used for treating diseases caused  
XX CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular  
XX CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-  
XX CC cell adhesion reactions, for treating cancer, or for inhibiting  
XX CC restenosis, particularly as antisense reagents. They are also useful in  
XX CC heterogeneous or homogeneous assays, as primers or probes, particularly  
XX CC where the target is amplified before being detected by hybridization, for  
XX CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain  
XX CC the increased affinity for complementary strands and better stability in  
XX CC serum, associated with conventional peptide nucleic acids (PNA), but lack  
XX CC the disadvantages, i.e. have improved cellular uptake, do not aggregate  
XX CC in aqueous solution, and have reduced affinity for purification  
XX CC materials, reduced cytotoxicity, better sequence specificity. They are  
XX CC more active than either DNA or PNA oligomers. When used as probes, (I)  
XX CC show different responses to base-pair mismatches in the DNA and PNA  
XX CC segments, allowing better discrimination between pathogenic and non-  
XX CC pathogenic conditions such as the transition from proto-oncogene to  
XX CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,  
XX CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme  
XX CC to be used to eliminate RNA or DNA primers. The DNA component allows  
XX CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)  
XX CC may be incorporated into a gene. AAH49208-AAH49264 represent  
XX CC oligonucleotides used to illustrate the method of the invention  
XX  
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
XX Best Local Similarity 90.0%; Pred. No. 37;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 CCTCATGATC 10  
XX | |||||  
XX 2 CATCATGATC 11  
XX  
Db 2 CATCATGATC 11  
XX  
RESULT 68  
AAH49256  
ID AAH49256 standard; DNA; 12 BP.  
XX

AC AAH49256;  
 XX 26-NOV-2001 (first entry)  
 XX PNA-forming oligonucleotide #19.  
 DE  
 XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
 XX antiviral; hepatocentric; vasotropic; antisense inhibition; ribozyme;  
 KM integrin; cell-cell adhesion; cancer; reestenosis; stability; PNA;  
 KM peptide nucleic acid; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP1113021-A2.  
 PD 04-JUL-2001.  
 PF 08-MAR-1995; 2001EP-00104012.  
 XX  
 PF 14-MAR-1994; 94DE-04408528.  
 XX  
 PR 08-MAR-1995; 95EP-00103332.  
 XX  
 PA (AVER ) AVENTIS PHARMA DEUT GMBH.  
 XX  
 PI Uhlmann E, Breipohl G;  
 XX  
 DR WPI; 2001-591267/67.  
 PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
 PT for treating e.g. cancer, also as diagnostic probes and primers.  
 XX  
 PS Example 43; Page 46; 54pp; German.

This invention describes novel polyamide-oligonucleotide derivatives (I) and their physiologically acceptable salts of formula  $F'(DNA)-Li_q(PNA-Li)_x(PNA-Li)_s(PNA-Li)_t$  where  $q, r, s, t = 0$  or 1, with the sum of two or more adjacent letters at least 2;  $x = 1-20$ ; DNA = nucleic acid (such as DNA or RNA or their known derivatives); Li = covalent linkage between DNA and PNA, i.e. a bond or a residue containing at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure containing at least one nucleobase different from thymine; and  $F' =$  end groups and/or are connected through a covalent bond. The products of the invention have anticancer, antiproliferative, antiviral, hepatocentric and vasotropic activity and can be used for the inhibition of gene expression by antisense, ribozyme, sense, or triple-helix methods, or by binding to proteins (aptamers). (I) are used for treating diseases caused by viruses (human immune deficiency, herpes simplex, influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-cell adhesion reactions, for treating cancer, or for inhibiting reestenosis, particularly as antisense reagents. They are also useful in heterogeneous or homogeneous assays, as primers or probes, particularly where the target is amplified before being detected by hybridization, for diagnosis of genetic, malignant or pathogen-related diseases. (I) retain the increased affinity for complementary strands and better stability in serum, associated with conventional peptide nucleic acids (PNA), but lack the disadvantages, i.e. have improved cellular uptake, do not aggregate in aqueous solution, and have reduced affinity for purification materials, reduced cytotoxicity, better sequence specificity. They are more active than either DNA or PNA oligomers. When used as probes, (I) show different responses to base-pair mismatches in the DNA and PNA segments, allowing better discrimination between pathogenic and non-pathogenic conditions such as the transition from proto-oncogene to oncogene, also, when used as primers, with the PNA segment at the 5'-end, they produce amplicons resistant to 5'-exonuclease, allowing this enzyme to be used to eliminate RNA or DNA primers. The DNA component allows additional reactions not possible with PNA alone, e.g. 3'-capping and (I) may be incorporated into a gene. AAH49208-AAH49264 represent oligonucleotides used to illustrate the method of the invention

Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 37;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10  
 |||||  
 DB 2 CATCATGTC 11

RESULT 69  
 AAH49260  
 ID AAH49260 standard; DNA; 12 BP.  
 XX  
 XX AAH49260;  
 AC  
 XX 26-NOV-2001 (first entry)  
 DT  
 XX PNA-forming oligonucleotide #23.  
 DE  
 XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
 KM antiviral; hepatocentric; vasotropic; antisense inhibition; ribozyme;  
 KM integrin; cell-cell adhesion; cancer; reestenosis; stability; PNA;  
 KM peptide nucleic acid; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP1113021-A2.  
 PD 04-JUL-2001.  
 PF 08-MAR-1995; 2001EP-00104012.  
 XX  
 PF 14-MAR-1994; 94DE-04408528.  
 XX  
 PR 08-MAR-1995; 95EP-00103332.  
 XX  
 PA (AVER ) AVENTIS PHARMA DEUT GMBH.  
 XX  
 PI Uhlmann E, Breipohl G;  
 XX  
 DR WPI; 2001-591267/67.  
 PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
 PT for treating e.g. cancer, also as diagnostic probes and primers.  
 XX  
 PS Example 43; Page 46; 54pp; German.

This invention describes novel polyamide-oligonucleotide derivatives (I) and their physiologically acceptable salts of formula  $F'(DNA)-Li_q(PNA-Li)_x(PNA-Li)_s(PNA-Li)_t$  where  $q, r, s, t = 0$  or 1, with the sum of two or more adjacent letters at least 2;  $x = 1-20$ ; DNA = nucleic acid (such as DNA or RNA or their known derivatives); Li = covalent linkage between DNA and PNA, i.e. a bond or a residue containing at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure containing at least one nucleobase different from thymine; and  $F' =$  end groups and/or are connected through a covalent bond. The products of the invention have anticancer, antiproliferative, antiviral, hepatocentric and vasotropic activity and can be used for the inhibition of gene expression by antisense, ribozyme, sense, or triple-helix methods, or by binding to proteins (aptamers). (I) are used for treating diseases caused by viruses (human immune deficiency, herpes simplex, influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-cell adhesion reactions, for treating cancer, or for inhibiting reestenosis, particularly as antisense reagents. They are also useful in heterogeneous or homogeneous assays, as primers or probes, particularly where the target is amplified before being detected by hybridization, for diagnosis of genetic, malignant or pathogen-related diseases. (I) retain the increased affinity for complementary strands and better stability in serum, associated with conventional peptide nucleic acids (PNA), but lack the disadvantages, i.e. have improved cellular uptake, do not aggregate in aqueous solution, and have reduced affinity for purification materials, reduced cytotoxicity, better sequence specificity. They are more active than either DNA or PNA oligomers. When used as probes, (I) show different responses to base-pair mismatches in the DNA and PNA segments, allowing better discrimination between pathogenic and non-pathogenic conditions such as the transition from proto-oncogene to

CC oncogene, also, when used as primers, with the PNA segment at the 5'-end.  
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme  
CC to be used to eliminate RNA or DNA primers. The DNA component allows  
CC additional reactions not possible with PNA alone, e.g. 3'-falling and (1)  
CC may be incorporated into a gene. AAH49208-AAH49264 represent  
CC oligonucleotides used to illustrate the method of the invention  
XX  
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCTCATGCTC 10  
2 CATCATGCTC 11  
DB 2 CCTCATGCTC 11  
RESULT 70  
AAH49261  
ID AAH49261 standard; DNA; 12 BP.  
XX  
AC AAH49261;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE PNA-forming oligonucleotide #24.  
XX  
KM Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
KM antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;  
KM integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;  
KM peptide nucleic acid; ss.  
XX  
OS Synthetic.  
XX  
PN BP1113021-A2.  
XX  
PD 04-JUL-2001.  
XX  
PF 08-MAR-1995; 2001EP-00104012.  
XX  
PR 14-MAR-1994; 94DE-04408528.  
PR 08-MAR-1995; 95EP-00103332.  
XX  
PA (AVERT ) AVENTIS PHARMA DEUT GMBH.  
XX  
PI Uhlmann E, Breipohl G;  
XX  
DR WPI; 2001-591267/67.  
XX  
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
PT for treating e.g. cancer, also as diagnostic probes and primers.  
XX  
PS Example 43; Page 46; 54pp; German.  
XX  
CC This invention describes novel polyamide-oligonucleotide derivatives (1)  
CC and their physiologically acceptable salts of formula F'(DNA)-Li<sub>q</sub>(PNA-  
CC Li) x (DNA-Li) s (PNA) t x<sup>r</sup> where q, r, s, t = 0 or 1, with the sum of  
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid  
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage  
CC between DNA and PNA, i.e. a bond or a residue containing at least one  
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure  
CC containing at least one nucleobase different from thymine, and F' =  
CC end groups and/or are connected through a covalent bond. The products of  
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic  
CC and vasotropic activity and can be used for the inhibition of gene  
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by  
CC binding to proteins (aptamers). (1) are used for treating diseases caused  
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular  
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-  
CC cell adhesion reactions, for treating cancer, or for inhibiting  
CC restenosis, particularly as antisense reagents. They are also useful in  
CC heterogeneous or homogeneous assays, as primers or probes, particularly

CC where the target is amplified before being detected by hybridization, for  
CC diagnosis of genetic, malignant or pathogen-related diseases. (1) retain  
CC the increased affinity for complementary strands and better stability in  
CC serum, associated with conventional peptide nucleic acids (PNA), but lack  
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate  
CC in aqueous solution, and have reduced affinity for purification  
CC materials, reduced cytotoxicity, better sequence specificity. They are  
CC more active than either DNA or PNA oligomers. When used as probes, (1)  
CC show different responses to base-pair mismatches in the DNA and PNA  
CC segments, allowing better discrimination between pathogenic and non-  
CC pathogenic conditions such as the transition from proto-oncogene to  
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,  
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme  
CC to be used to eliminate RNA or DNA primers. The DNA component allows  
CC additional reactions not possible with PNA alone, e.g. 3'-falling and (1)  
CC may be incorporated into a gene. AAH49208-AAH49264 represent  
CC oligonucleotides used to illustrate the method of the invention  
XX  
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCTCATGCTC 10  
2 CATCATGCTC 11  
DB 2 CCTCATGCTC 11  
RESULT 71  
AAH49259  
ID AAH49259 standard; DNA; 12 BP.  
XX  
AC AAH49259;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE PNA-forming oligonucleotide #22.  
XX  
KM Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
KM antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;  
KM integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;  
KM peptide nucleic acid; ss.  
XX  
OS Synthetic.  
XX  
PN BP1113021-A2.  
XX  
PD 04-JUL-2001.  
XX  
PF 08-MAR-1995; 2001EP-00104012.  
XX  
PR 14-MAR-1994; 94DE-04408528.  
PR 08-MAR-1995; 95EP-00103332.  
XX  
PA (AVERT ) AVENTIS PHARMA DEUT GMBH.  
XX  
PI Uhlmann E, Breipohl G;  
XX  
DR WPI; 2001-591267/67.  
XX  
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
PT for treating e.g. cancer, also as diagnostic probes and primers.  
XX  
PS Example 43; Page 46; 54pp; German.  
XX  
CC This invention describes novel polyamide-oligonucleotide derivatives (1)  
CC and their physiologically acceptable salts of formula F'(DNA)-Li<sub>q</sub>(PNA-  
CC Li) x (DNA-Li) s (PNA) t x<sup>r</sup> where q, r, s, t = 0 or 1, with the sum of  
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid  
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage  
CC between DNA and PNA, i.e. a bond or a residue containing at least one  
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure



PR 11-APR-2000; 2000US-00547735.  
XX (COGE-) COGENT NEUROSCIENCE INC.  
XX  
XX  
PI Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC, Barney S;  
XX WPI; 2002-025874/03.  
XX  
XX  
PT New protective sequences and their products, useful for diagnosing and  
PT treating diseases involving cell death, including neurological disorders  
PT e.g. stroke and for identifying modulators of expression of the  
PT protective sequences.  
XX  
XX  
PS Claim 2; Fig 5; 283pp; English.  
XX  
XX The present invention relates to protective sequence proteins (ABBA4624-  
CC ABB44830) and their coding sequences (ABBA2701-ABBA2937). The sequences,  
CC when introduced into a cell either predisposed to undergo cell death or  
CC in the process of undergoing cell death, prevent, delay or rescue the  
CC cell from death, hence, these sequences are named "protective sequences".  
CC The sequences are useful for treating and/or ameliorating cancer,  
CC autoimmune diseases and neurological disorders e.g. stroke. Further  
CC examples of diseases which may be treated by the present invention are  
CC given in the specification  
XX  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CTCATGCTCA 11  
DB 11 CACATGCTCA 2  
  
RESULT 74  
ABK72560  
ID ABK72560 standard; DNA; 12 BP.  
XX  
XX ABK72560;  
AC  
XX  
DT 13-AUG-2002 (first entry)  
XX  
XX Human OPA1 gene, exon/intron junction #27.  
DE  
XX Human; ophthalmological; OPA1; autosomal dominant optic atrophy; ADOA;  
KM gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200227022-A2.  
PN  
XX  
XX 04-APR-2002.  
PD  
XX  
XX 26-SEP-2001; 2001WO-GB004284.  
PF  
XX  
XX 26-SEP-2000; 2000GB-00023555.  
PR  
XX  
XX (UNLCO ) UNIV COLLEGE LONDON.  
PA (UYEX-) UNIV EYE HOSPITAL.  
XX  
XX Bhattacharya S, Wissinger B, Alexander C, Votruba M;  
PI WPI; 2002-416484/44.  
XX  
XX  
XX Novel human normal or mutant OPA1 (the predominant locus for autosomal  
PT dominant optic atrophy (ADOA)) polypeptides and the OPA1 gene, useful in  
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
XX  
XX Disclosure; Fig 12; 75pp; English.  
XX  
XX The invention relates to an isolated human normal or mutant OPA1 (the

CC predominant locus for autosomal dominant optic atrophy (ADOA))  
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,  
CC and substantially free of other human proteins. Also described is the DNA  
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the  
CC treatment of a medical condition resulting from a defect in the OPA1  
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid  
CC and antibodies to (I) are useful in a variety of hybridisation and  
CC immunological assays to screen for, and to detect the presence of, either  
CC a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593  
CC represent the human OPA1 gene and intron/exon splice junctions  
XX  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TCACATGAT 18  
DB 3 TCACATGAT 12  
  
RESULT 75  
ABA01332/C  
ID ABA01332 standard; RNA; 12 BP.  
XX  
XX ABA01332;  
AC  
XX  
XX 29-AUG-2003 (revised)  
DT  
XX 03-JUL-2002 (first entry)  
DT  
XX  
XX HIV-1 rev oligonucleotide #5.  
DE  
XX  
XX Selenoprotein; HIV; Ebola virus; cancer; immune system disorder; ss.  
KM  
XX Human immunodeficiency virus 1.  
OS  
XX  
XX US6303295-B1.  
PN  
XX  
XX 16-OCT-2001.  
PD  
XX  
XX 12-JUL-1996; 96US-00679493.  
PF  
XX  
XX 14-JUL-1995; 95US-0001203P.  
PR  
XX 01-SEP-1995; 95US-0003112P.  
XX  
XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA  
XX  
XX Taylor EW, Nadiimpalli RG, Ramanathan CS;  
PI WPI; 2002-024734/03.  
XX  
XX  
XX New selenoprotein for use in detecting certain viruses, e.g. human  
PT immunodeficiency virus (HIV) or Ebola, cancer and immune system  
PT disorders.  
XX  
XX Disclosure; Col 26; 140pp; English.  
PS  
XX  
XX The present invention relates to selenoproteins encoded in the genome of  
CC a virus, where the coding sequence of the selenoprotein is genetically  
CC engineered for expression in a nucleic acid construct. The invention also  
CC discloses a method for identifying selenoprotein coding sequences, for  
CC detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
CC disorders. The present sequence was used to illustrate the invention.  
XX (Updated on 29-AUG-2003 to standardise OS field)  
XX  
XX  
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 0 T; 2 U; 0 Other;  
  
Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CTCATGCTCA 11

```
Db          11 CTCAGGCTCA 2
RESULT 76
AAK96610
ID AAK96610 standard; DNA; 12 BP.
XX
XX AAK96610;
AC
XX 16-APR-2002 (first entry)
XX
XX Modified peptide nucleic acid #1.
XX
XX Peptide nucleic acid; PNA; polyamide backbone; phosphoryl radical;
XX cytosatic; virucide; dermatological; antiaesthetic; cancer; antisense;
XX viral infection; vitiligo; pigmentation disorder; asthma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /mod_base= OTHER
XX /note="modified by phosphate and N-(2-
XX modified_base 12
XX hydroxyethyl)glycine"
XX /*tag= b
XX /mod_base= OTHER
XX /note="modified by hex"
XX
XX WO200179249-A2.
XX
XX 25-OCT-2001.
XX
XX 07-APR-2001; 2001WO-EP004027.
XX
XX 18-APR-2000; 2000DE-01019136.
XX
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
XX Uhlmann E, Breipohl G, Will DW;
XX
XX MPI; 2002-089643/12.
XX
XX New peptide nucleic acid derivatives, useful e.g. for treating tumors and
XX diagnosis, have N-terminal phosphoryl residue for improving e.g.
XX solubility in water.
XX
XX Example 3; Page 38; 96pp; German.
XX
XX The present invention relates to peptide nucleic acid (PNA) derivatives.
XX These can be used in the treatment of cancer, viral infections, vitiligo
XX or other pigmentation disorders, and asthma. The present sequence is an
XX oligonucleotide fragment of a PNA described in the exemplification of the
XX invention
XX
XX Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTCATGCTC 10
DB 2 CATCATGCTC 11
RESULT 77
ABA97503
ID ABA97503 standard; DNA; 12 BP.
XX
XX ABA97503;
```

```
XX
XX 16-APR-2002 (first entry)
XX
XX Peptide nucleic acid SEQ ID NO: 50.
XX
XX Peptide nucleic acid; PNA; polyamide backbone; phosphoryl radical;
XX cytosatic; virucide; dermatological; antiaesthetic; cancer; antisense;
XX viral infection; vitiligo; pigmentation disorder; asthma; ss.
XX
XX Synthetic.
XX
XX WO200179249-A2.
XX
XX 25-OCT-2001.
XX
XX 07-APR-2001; 2001WO-EP004027.
XX
XX 18-APR-2000; 2000DE-01019136.
XX
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
XX Uhlmann E, Breipohl G, Will DW;
XX
XX MPI; 2002-089643/12.
XX
XX New peptide nucleic acid derivatives, useful e.g. for treating tumors and
XX diagnosis, have N-terminal phosphoryl residue for improving e.g.
XX solubility in water.
XX
XX Disclosure; Page 91; 96pp; German.
XX
XX The present invention relates to peptide nucleic acid (PNA) derivatives.
XX These can be used in the treatment of cancer, viral infections, vitiligo
XX or other pigmentation disorders, and asthma. The present sequence is an
XX oligonucleotide fragment of a PNA described in the exemplification of the
XX invention
XX
XX Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTCATGCTC 10
DB 2 CATCATGCTC 11
RESULT 78
ADM56294/C
ID ADM56294 standard; DNA; 12 BP.
XX
XX ADM56294;
AC
XX 03-JUN-2004 (first entry)
XX
XX Mouse SLC26A6 anion transporter protein gene splice site #13.
XX
XX SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;
XX splice site; ds; mouse; murine.
XX
XX Mus musculus.
XX
XX WO2003072759-A2.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006469.
XX
XX 28-FEB-2002; 2002US-0360275P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX
XX
```

PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 XX  
 PI Mount DB, Romero MF;  
 XX  
 DR MPI; 2003-712726/67.  
 XX  
 PT New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing a  
 PT competition for treating e.g., cancer.  
 XX  
 PS Example 2; SEQ ID NO 26; 204pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequences of SLC26A6,  
 CC SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein  
 CC sequences of the invention are useful for treating cancer. The present  
 CC DNA sequence represents a splice site from the gene encoding the mouse  
 CC SLC26A6 anion transporter protein.  
 XX  
 SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 42.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 37;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 TCACATGAT 18  
 DB 10 TCACATGAT 1  
 XX  
 RESULT 79  
 ADQ29965  
 ID ADQ29965 standard; DNA; 12 BP.  
 XX  
 AC ADQ29965;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Rat VR1 exon 1d transcription factor binding fragment #41.  
 XX  
 KW ds; VR1 receptor; vanilloid receptor type 1; modulator;  
 KW pain transmission; primary sensory neuron; transcription factor;  
 KW detection; MZFI; NKAPPAB; NFAT; GATA1; sensitivity disorder; analgesia;  
 KW hyperalgesia; hyperalgesia; neuralgia; myalgia; rat.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO2004053120-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 01-DEC-2003; 2003WO-EF013522.  
 XX  
 PR 09-DEC-2002; 2002DE-01057421.  
 XX  
 PA (CHER ) GRUENTHAL GMBH.  
 XX  
 PI Weihe E, Bieller A, Schaefer MKH;  
 XX  
 DR MPI; 2004-468868/44.  
 XX  
 PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
 PT useful for control of pain or sensitivity disorders, comprises sequences  
 PT from control regions of the receptor gene.  
 XX  
 PS Disclosure; Page 46; 68pp; German.  
 XX  
 CC This invention describes a novel nucleic acid containing a specific  
 CC segment having at least one region that modulates expression of the VR1  
 CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
 CC or fragment of this region, or a sequence that hybridizes to it under  
 CC standard conditions. The VR1 modulator is derived from one or more of  
 CC positions 221931-22344 of GenBank AL670399, 31673-36359 of AL663116, or  
 CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
 CC pain, particularly in primary sensory neurons. The invention also

CC describes a vector that contains the VR1 modulator, host cells containing  
 CC this vector (other than human germ or embryonal stem cells) and a method  
 CC for modulating expression of the VR1 receptor by introducing the  
 CC modulator or the vector into a cell that contains the VR1 gene. The  
 CC products of the invention are used for detecting a transcription factor  
 CC from its binding to a regulatory sequence (or a double-stranded  
 CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
 CC linked immunosorbent assay, particularly for diagnosis of diseases  
 CC associated with overexpression or underexpression of the transcription  
 CC factor. The region that modulates VR1 receptor expression includes a  
 CC binding site for a transcription factor, e.g. MZFI, NKAPPAB, NFAT or  
 CC GATA1. The nucleic acids of the invention, or vectors containing them,  
 CC are used for prevention or treatment of pain, also for treating them,  
 CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also  
 CC neuralgia and myalgia, that are associated with activity of the VR1  
 CC receptor. This sequence represents a fragment of rat VR1 exon 1d DNA  
 CC which is capable of binding to a transcription factor.  
 XX  
 SQ Sequence 12 BP; 3 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 42.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 37;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 CACATGGATG 19  
 DB 1 CACATGGATG 10  
 XX  
 RESULT 80  
 AEF80873/C  
 ID AEF80873 standard; DNA; 12 BP.  
 XX  
 AC AEF80873;  
 XX  
 DT 20-APR-2006 (first entry)  
 XX  
 DE MLTF/USF promoter target DNA fragment.  
 XX  
 KW Gene expression; gene regulation; platinum zinc complex; cancer; tumor;  
 KW neoplasm; promoter; target; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2006045131-A.  
 XX  
 PD 16-FEB-2006.  
 XX  
 PF 05-AUG-2004; 2004JP-00229182.  
 XX  
 PR 05-AUG-2004; 2004JP-00229182.  
 XX  
 PA (UYTK ) UNIV TOKYO RIKA GH.  
 XX  
 PI Aoki S, Okaya R, Takeda T, Kimura E;  
 XX  
 DR MPI; 2006-150505/16.  
 XX  
 PT Novel platinum-zinc complex useful as agent for controlling expression of  
 PT promoter sequence or RNA of specific gene for treatment of cancer.  
 XX  
 PS Example 4; Page 10; 21pp; Japanese.  
 XX  
 CC The invention relates to a novel platinum-zinc complex (C1) used in the  
 CC regulation of gene expression. The complex of the invention is prepared  
 CC by reacting a 2,2'-bipyridyl derivative and a cyclen derivative protected  
 CC by t-butyloxycarbonyl (Boc), adding the platinum compound to the obtained  
 CC complex. (C1) is useful as an agent for controlling the expression of a  
 CC specific gene. This involves contacting (C1) with the nucleic acid  
 CC sequence of the gene, where the nucleic acid sequence is a promoter  
 CC sequence which controls the expression of the gene, or an RNA encoding  
 CC the gene. The platinum complex in (C1) has increased anti-tumor activity  
 CC with respect to solid tumors such as testicular tumors, ovarian cancer,

CC head and neck cancer, esophageal cancer and small cell lung carcinoma.  
CC (C1) controls the gene expression by the combination of zinc and platinum  
CC complex in its structure. The current sequence represents a promoter  
CC fragment that may act as a target for the complex of the invention.  
XX

SQ Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 37;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGTCACATGG 16  
|||||

Db 12 GGTCACATGG 3

Search completed: June 13, 2006, 15:46:02  
Job time : 0.001 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:44:11 ; Search time 0.001 Seconds

(without alignments)  
18.680 Million cell updates/sec

Title: US-10-719-370A-446

Perfect score: 20

Sequence: 1 cctcatgctcacatgatga 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 36 seqs, 467 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 12

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 36 summaries

Database : us-10-719-370a-446.sl.rge4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	85.0	20	1	ACCESSION:CS097426
C 2	14.8	74.0	19	1	AR199401
C 3	12.8	64.0	17	1	AX732438
C 4	12.2	61.0	17	1	CO622872
C 5	12.2	61.0	17	1	AR463935
C 6	10.8	54.0	15	1	AR180445
C 7	9.4	47.0	15	1	A71522
C 8	9.4	47.0	13	1	S74610
C 9	9.4	47.0	13	1	AR759769
C 10	9.4	47.0	13	1	AR759770
C 11	9.4	45.0	13	1	AR058623
C 12	8.8	44.0	12	1	I04322
C 13	8.4	42.0	12	1	AR024074
C 14	8.4	42.0	12	1	AR075457
C 15	8.4	42.0	12	1	AR108947
C 16	8.4	42.0	12	1	AR153908
C 17	8.4	42.0	12	1	AR172244
C 18	8.4	42.0	12	1	AR178525
C 19	8.4	42.0	12	1	BD001178
C 20	8.4	42.0	12	1	BD001607
C 21	8.4	42.0	12	1	BD064941
C 22	8.4	42.0	12	1	BD240723
C 23	8.4	42.0	12	1	BD261806
C 24	8.4	42.0	12	1	BD261806
C 25	8.4	42.0	12	1	CO828540
C 26	8.4	42.0	12	1	I17542
C 27	8.4	42.0	12	1	AR224293
C 28	8.4	42.0	12	1	AR234464
C 29	8.4	42.0	12	1	AR275829
C 30	8.4	42.0	12	1	I58612
C 31	8.4	42.0	12	1	I72395
C 32	8.4	42.0	12	1	AR577337
C 33	8.4	42.0	12	1	AR699868
					ACCESSION:AR699877

C 34	8.4	42.0	12	1	AR699878	ACCESSION:AR699878
C 35	8.4	42.0	12	1	AX283286	ACCESSION:AX283286
C 36	8.4	42.0	12	1	AX711060	ACCESSION:AX711060

## ALIGNMENTS

## RESULT 1

CS097426/c

LOCUS CS097426 20 bp DNA linear PAT 03-JUN-2005

DEFINITION Sequence 69 from Patent WO2005045070.

ACCESSION CS097426

VERSION CS097426.1 GI:66953875

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BIOREFERENCE

FEATURES

source

1. .20

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match

Best Local Similarity 85.0%; Score 17; DB 1;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CCTCATGCTCACATGGA 1

RESULT 2

AR199401

LOCUS AR199401 19 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 22 from patent US 6355434.

ACCESSION AR199401

VERSION AR199401.1 GI:20249475

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .19

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

Query Match

Best Local Similarity 74.0%; Score 14.8; DB 1; Length 19;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 CTTCATGCTCACATGATG 19

RESULT 3

AX732438/c

LOCUS AX732438 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 4072 from Patent WO03025175.

ACCESSION AX732438  
VERSION AX732438.1 GI:30511781  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Telerman, A., Amson, R. and Tullinder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 4072 27-MAR-2003;  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 64.0%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.3;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 3 TCATGTCACATGAT 18  
Db 17 TCAGGTCAATGAT 2  
RESULT 4  
LOCUS CQ622872 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 7612 from Patent WO0192524.  
ACCESSION CQ622872  
VERSION CQ622872.1 GI:41673090  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E. Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 7612 06-DEC-2001;  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 61.0%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 4.5;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 CCTCATGTCACATGGA 17  
Db 17 CCTCAAGTCACAGTA 1  
RESULT 5  
LOCUS AR463935 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 7612 from patent US 6686188.  
ACCESSION AR463935  
VERSION AR463935.1 GI:42689992  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 7612 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source  
1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 61.0%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 4.5;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 CCTCATGTCACATGGA 17  
Db 17 CCTCAAGTCACAGTA 1  
RESULT 6  
LOCUS AR180445 15 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 513 from patent US 6333152.  
ACCESSION AR180445  
VERSION AR180445.1 GI:20222478  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 15)  
AUTHORS Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W. Gene expression profiles in normal and cancer cells  
JOURNAL Patent: US 6333152-A 513 25-DEC-2001;  
FEATURES  
source  
1. .15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 54.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 6.8;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 CATGTCACATGGA 17  
Db 1 CATGCCACATGGA 14  
RESULT 7  
LOCUS A71522 12 bp DNA linear PAT 07-MAY-1999  
DEFINITION Sequence 81 from Patent WO9813521.  
ACCESSION A71522  
VERSION A71522.1 GI:4775134  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
Unclassified sequences.  
REFERENCE  
1 (bases 1 to 12)  
AUTHORS Fesce, R. and Consalez, G. METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM PRIMER REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION  
JOURNAL Patent: WO 9813521-A 81 02-APR-1998;  
FESCE RICCARDO (IT)  
FEATURES  
source  
1. .12  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 47.0%; Score 9.4; DB 1; Length 12;

Best Local Similarity 90.9%; Pred. No. 8.2;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCGTCACATGG 16  
Db 2 TCGTCACATGG 12

## RESULT 8

S74610

LOCUS 12 bp mRNA linear PRI 07-MAY-1993  
DEFINITION lipoprotein lipase (exon 2-exon 3 boundary) [human, mRNA Partial  
Mutant, 12 nt].

S74610

S74610.1 GI:241423

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REMARK

FEATURES

source

gene

CDS

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
1.12  
/gene="lipoprotein lipase, LPL"  
1.12  
/gene="lipoprotein lipase, LPL"  
/note="contains in-frame 18-base pair deletion; LPL"  
/codon\_start=1  
/product="lipoprotein lipase"  
/protein\_id="AAB20748.1"  
/db\_xref="GI:241424"  
/translation="FMVT"

Query Match 47.0%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 8.2;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGTCACATGG 13  
Db 2 TCGTCACATGG 12

## RESULT 9

AR759769

LOCUS 13 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 12 from patent US 6958240.  
ACCESSION AR759769  
VERSION AR759769.1 GI:83326505  
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Unknown.  
Unclassified.  
1 (bases 1 to 13)  
Baird, E.E. and Dervan, P.B.  
Inhibition of major groove DNA binding proteins by modified  
polyamides  
Patent: US 6958240-A 12-25-OCT-2005;  
California Institute of Technology; Pasadena, CA  
Location/Qualifiers  
1.13

/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 47.0%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 9.8;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGTCACATGG 13  
Db 3 TCGTCACATGG 13

## RESULT 10

AR759770/c

LOCUS 13 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 13 from patent US 6958240.  
ACCESSION AR759770  
VERSION AR759770.1 GI:83326506  
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REMARK

FEATURES

source

gene

CDS

Query Match 47.0%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 9.8;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGTCACATGG 13  
Db 1 TCGTCACATGG 1

## RESULT 11

AR058623/c

LOCUS 12 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 200 from patent US 5837832.  
ACCESSION AR058623  
VERSION AR058623.1 GI:5984200  
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Unknown.  
Unclassified.  
1 (bases 1 to 12)  
Chee, M., Cronin, M.T., Fodor, S.P.A., Huang, X.X., Hubbell, E.A.,  
Lipshutz, R.J., Lobban, P.E., Morris, M.S. and Shaldon, E.L.  
Arrays of nucleic acid probes on biological chips  
Patent: US 5837832-A 200 17-NOV-1998;  
Location/Qualifiers  
1.12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 45.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CATGATGA 20  
Db 11 CATGATGA 3

## RESULT 12

I04322

LOCUS I04322 12 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 7 from Patent EP 0147819.  
ACCESSION I04322  
VERSION I04322.1 GI:591774  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kung,H.-F. and Yamazaki,S.  
TITLE Purification of recombinant Interleukin-2  
JOURNAL Patent: EP 0147819-A2 7 10-JUL-1985;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TGGTCACATGGA 17  
| | | | | | | | | |  
Db 1 TTGTCACTGCGA 12

RESULT 13  
AR024074/c AR024074 12 bp DNA linear PAT 05-DEC-1998  
LOCUS AR024074  
DEFINITION Sequence 24 from patent US 5795778.  
ACCESSION AR024074  
VERSION AR024074.1 GI:3977368  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting herpes simplex virus replication  
JOURNAL Patent: US 5795778-A 24 18-AUG-1998;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGCTCAC 12  
| | | | | | | | | |  
Db 12 TCATGCTCAC 3

RESULT 14  
AR075457/c AR075457 12 bp DNA linear PAT 30-AUG-2000  
LOCUS AR075457  
DEFINITION Sequence 10 from patent US 5958424.  
ACCESSION AR075457  
VERSION AR075457.1 GI:10002207  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Noteborn,M.H.M. and De Boer,G.F.  
TITLE Recombinant chicken anemia virus particle  
JOURNAL Patent: US 5958424-A 10 28-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGCG 16  
| | | | | | | | | |  
Db 12 GGTCACTGCG 3

RESULT 15  
AR108947/c AR108947 12 bp DNA linear PAT 14-FEB-2001  
LOCUS AR108947  
DEFINITION Sequence 2 from patent US 6113913.  
ACCESSION AR108947  
VERSION AR108947.1 GI:12825223  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Brough,D.E. and Kovesdi,I.  
TITLE Recombinant adenovirus  
JOURNAL Patent: US 6113913-A 2 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGCG 16  
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Db 12 GGTCACTGCG 3

RESULT 16  
AR153908/c AR153908 12 bp DNA linear PAT 08-AUG-2001  
LOCUS AR153908  
DEFINITION Sequence 10 from patent US 6238669.  
ACCESSION AR153908  
VERSION AR153908.1 GI:15121961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Noteborn,M.H.M. and De Boer,G.F.  
TITLE Proteins encoded by chicken anemia virus DNA and diagnostic kits  
JOURNAL Patent: US 6238669-A 10 29-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTGCG 16  
| | | | | | | | | |  
Db 12 GGTCACTGCG 3

RESULT 17  
AR172244/c AR172244 12 bp DNA linear PAT 17-DEC-2001  
LOCUS AR172244  
DEFINITION Sequence 68 from patent US 6303295.  
ACCESSION AR172244  
VERSION AR172244.1 GI:17911735  
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Taylor,E.Will., Nadiimpalli,R.Gopal, and Ramanathan,C.Sekar.
TITLE        Selenoproteins, coding sequences and methods
JOURNAL      Patent: US 6303295-A 68 16-OCT-2001;
FEATURES     Location/Qualifiers
SOURCE       1..12
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 13;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTCATGTCGA 11
        |||||
        11 CTCAGGTCGA 2

RESULT 18
LOCUS     AR178525               12 bp    DNA    linear    PAT 20-APR-2002
DEFINITION Sequence 10 from patent US 6319693.
ACCESSION AR178525
VERSION   AR178525.1 GI:20219663
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Noteborn,M.H.M, and de Boer,G.F.
TITLES    Cloning of chicken anemia virus DNA
JOURNAL    Patent: US 6319693-A 10 20-NOV-2001;
FEATURES   Location/Qualifiers
SOURCE     1..12
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 13;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GGTACATCG 16
        |||||
        12 GGTACGTCG 3

RESULT 19
LOCUS     BD001178               12 bp    RNA    linear    PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001178
VERSION   BD001178.1 GI:18625737
KEYWORDS  JP 2000342285-A/338.
SOURCE    synthetic construct
           other sequences; artificial sequences.
           1 (bases 1 to 12)
REFERENCE Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
AUTHORS   Holasek,J.J. and Mamone,A.J.
TITLE      Method and reagent for inhibiting viral replication
JOURNAL    Patent: JP 2000342285-A 338 12-DEC-2000;
FEATURES   RIBOZYME PHARMACEUTICALS INC
SOURCE     OS Artificial Sequence
           PN JP 2000342285-A/338
           PD 12-DEC-2000
           PR 01-MAY-2000 JP 2000132616
           PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
           14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
           14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
           14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR

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14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884521 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK.
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22//C12N5/10, C12R1:91, PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
CC
FH Key 1..12 Location/Qualifiers
FT source 1..12 /organism='Artificial Sequence'.

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Query Match      42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 13;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCATGTCAC 12
        |||||
        12 TCATGTCAC 3

RESULT 20
LOCUS     BD001607               12 bp    RNA    linear    PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001607
VERSION   BD001607.1 GI:18626166
KEYWORDS  JP 2000342286-A/338.
SOURCE    synthetic construct
           other sequences; artificial sequences.
           1 (bases 1 to 12)
REFERENCE Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
AUTHORS   Holasek,J.J. and Mamone,A.J.
TITLE      Method and reagent for inhibiting viral replication
JOURNAL    Patent: JP 2000342286-A 338 12-DEC-2000;
FEATURES   RIBOZYME PHARMACEUTICALS INC
SOURCE     OS Artificial Sequence
           PN JP 2000342286-A/338
           PD 12-DEC-2000
           PR 01-MAY-2000 JP 2000132651
           PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
           14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
           14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
           14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
           14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
           14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
           14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
           14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
           14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884521 PR
           14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
           31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
           26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
           15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
           07/987130,07-DEC-1992 US 07/987133 PI
           KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
           MAYSEJAK,
           PI JAMES J HOLESEK, ANTHONY J MAMONE
           PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,

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PC A61K39/135,  
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,  
PC A61P1/16,  
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC  
(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC  
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CC  
FH Key Location/Qualifiers  
FT source 1..12  
FT /organism='Artificial Sequence',  
Location/Qualifiers  
1..12  
/organism='synthetic construct'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32630'

FEATURES  
source

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Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGCTCAC 12  
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Db 12 TCATGCTCAC 3

RESULT 21  
LOCUS BD064941/c 12 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for detecting the extent of binding of transcriptional  
regulatory protein to oligoDNA.  
ACCESSION BD064941  
VERSION BD064941.1 GI:22610544  
KEYWORDS JP 2001275678-A/153.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 12)  
Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Minaki, Fukushima,R. and  
Minikawa,K.,  
TITLE Method for detecting the extent of binding of transcriptional  
regulatory protein to oligoDNA  
JOURNAL Patent: JP 2001275678-A 153 09-OCT-2001;  
SUMITOMO ELECTRIC INDUSTRIES LTD  
COMMENT OS Artificial Sequence  
PN JP 2001275678-A/153  
PD 09-OCT-2001  
PF 31-MAR-2000 JP 2000096306  
PI TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI  
MIMAKI,REI FUKUSHIMA,  
PI KAZUKO NISHIKAWA  
PC C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC  
Synthetic DNA  
FH Key Location/Qualifiers  
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Location/Qualifiers  
1..12  
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/db\_xref='taxon:32630'

FEATURES  
source

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTG 16  
|||||  
Db 12 GGTCACTG 3

RESULT 22  
LOCUS BD240723/c 12 bp DNA linear PAT 17-JUL-2003

DEFINITION Replication-deficient recombinant adenovirus having mutation major  
late promoter.  
ACCESSION BD240723  
VERSION BD240723.1 GI:33050493  
KEYWORDS JP 2002519036-A/2.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 12)  
Brough,D.E. and Kovsed,I.  
AUTHORS Brough,D.E. and Kovsed,I.  
TITLE Replication-deficient recombinant adenovirus having mutation major  
late promoter  
JOURNAL Patent: JP 2002519036-A 2 02-JUL-2002;  
GENVEC, INC  
COMMENT OS Human adenovirus serotype 5  
PN JP 2002519036-A/2  
PD 02-JUL-2002  
PF 24-JUN-1999 JP 2000557381  
PR 26-JUN-1998 US 09/105515  
PI DOUGLAS E BROUGH,IMRE KOVSEDI  
PC C12N15/09,C12N5/10,C12N7/00//A61K35/76,A61K39/235,A61K48/00,  
PC C12N15/00,  
PC C12N5/00  
CC Replication-deficient recombinant adenovirus having mutation  
CC promoter major late  
CC  
FH Key Location/Qualifiers  
FT source 1..12  
FT /organism='Human adenovirus serotype 5',  
Location/Qualifiers  
1..12  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

FEATURES  
source

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACTG 16  
|||||  
Db 12 GGTCACTG 3

RESULT 23  
LOCUS BD261806 12 bp DNA linear PAT 17-JUL-2003  
DEFINITION Enhancement in protein production by higher plants using ubiquitin  
or cucumber mosaic virus coating protein peptide.  
ACCESSION BD261806  
VERSION BD261806.1 GI:33071574  
KEYWORDS JP 2002532098-A/10.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 12)  
Fang,R.X., Wu,J.L. and Chen,X.Y.  
AUTHORS Enhancement in protein production by higher plants using ubiquitin  
or cucumber mosaic virus coating protein peptide  
JOURNAL Patent: JP 2002532098-A 10 02-OCT-2002;  
INSTITUTE OF MOLECULAR AGROBIOLOGY  
COMMENT OS Plasmid pCL  
PN JP 2002532098-A/10  
PD 02-OCT-2002  
PF 11-DEC-1998 JP 2000588378  
PI RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN  
PC C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC  
C12N5/00  
CC Joining region between fusion of genes.  
FH Key Location/Qualifiers  
FT misc\_feature (1)..(12).  
FT Location/Qualifiers  
1..12

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Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GTCACATGGA 17
Db 2 GTCGACATGGA 11

RESULT 24
LOCUS CQ828540 12 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 258 from Patent WO2004053120.
ACCESSION CQ828540
VERSION CQ828540.1 GI:49732023
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE
1 Weihe, E., Bieller, A. and Schaefer, M.K.
Regulatory elements in the 5' region of the vrl gene
Patent: WO 2004053120-A 258 24-JUN-2004;
Gruenthal GmbH (DE)
FEATURES
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/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
/note="V$IK2 01"

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CACATGATG 19
Db 1 CACAGGATG 10

RESULT 25
LOCUS I17542 12 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 10 from patent US 5491073.
ACCESSION I17542
VERSION I17542.1 GI:1597897
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Noteborn, M.H.M. and de Boer, G.F.
TITLE Cloning of chicken anaemia DNA
JOURNAL Patent: US 5491073-A 10 13-FEB-1996;
FEATURES
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGTCAATGG 16
Db 12 GGTCAATGG 3
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RESULT 26
LOCUS AR224293/C 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 24 from patent US 6440719.
ACCESSION AR224293
VERSION AR224293.1 GI:23333070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Draper, K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 24 27-AUG-2002;
Ribozyme Pharmaceuticals, Inc.; Boulder, CO
FEATURES
source 1..12
/organism="unknown"
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Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCATGTCAC 12
Db 12 TCATGCCAC 3

RESULT 27
LOCUS AR234464/C 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6458578.
ACCESSION AR234464
VERSION AR234464.1 GI:27277166
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Brough, D.B. and Kovsed, I.
TITLE Recombinant cell line produces adenoviral gene products E1 and
JOURNAL DEF-A, and/or DEF-B
Patent: US 6458578-A 2 01-OCT-2002;
Genvec, Inc.; Gaithersburg, MD
FEATURES
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGTCAATGG 16
Db 12 GGTCAATGG 3

RESULT 28
LOCUS AR275829/C 12 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 10 from patent US 6509446.
ACCESSION AR275829
VERSION AR275829.1 GI:29709474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Noteborn, M.H.M. and De Boer, G.F.
TITLE Cloning of chicken anaemia DNA
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JOURNAL Patent: US 6509446-A 10 21-JAN-2003;

Lead B.V.; Leiden;

NLX;

FEATURES Location/Qualifiers

source

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Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 13;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16

Db 12 GGTCACGTGG 3

RESULT 29

LOCUS I58612

DEFINITION Sequence 3 from patent US 5652144. 12 bp DNA 1linear PAT 07-OCT-1997

ACCESSION I58612

VERSION I58612.1 GI:2477850

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE Unclassified.

1 (bases 1 to 12)

AUTHORS Lu, Y. and Haseltine, W.A.

TITLE YCI gene

JOURNAL Patent: US 5652144-A 3 29-JUL-1997;

FEATURES Location/Qualifiers

source 1. .12

/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 13;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16

Db 12 GGTCACGTGG 3

RESULT 30

LOCUS I72395/c

DEFINITION Sequence 26 from patent US 5683985. 12 bp DNA 1linear PAT 03-APR-1998

ACCESSION I72395

VERSION I72395.1 GI:3008534

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE Unclassified.

1 (bases 1 to 12)

AUTHORS Chu B.Chen, Pei, and Orgel, L.

TITLE Oligonucleotide decays and methods relating thereto

JOURNAL Patent: US 5683985-A 26 04-NOV-1997;

FEATURES Location/Qualifiers

source 1. .12

/organism="unknown"  
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Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 13;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGTCACATGG 16

Db 12 GGTCACGTGG 3

RESULT 31

LOCUS AR577337

DEFINITION Sequence 54 from patent US 6777544. 12 bp DNA 1linear PAT 14-DEC-2004

ACCESSION AR577337

VERSION AR577337.1 GI:56579871

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE Unclassified.

1 (bases 1 to 12)

AUTHORS Uhlmann, E., Breipohl, G. and Will, D.W.

TITLE Polyamide nucleic acid derivatives and agents and processes for

preparing them

JOURNAL Patent: US 6777544-A 54 17-AUG-2004;

Aventis Pharma Deutschland GmbH; Frankfurt;

DEX;

FEATURES

source Location/Qualifiers

1. .12  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 13;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGCTC 10

Db 2 CATCATGCTC 11

RESULT 32

LOCUS AR699868

DEFINITION Sequence 38 from patent US 6919441. 12 bp DNA 1linear PAT 14-SEP-2005

ACCESSION AR699868

VERSION AR699868.1 GI:75205772

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE Unclassified.

1 (bases 1 to 12)

AUTHORS Uhlmann, E. and Breipohl, G.

TITLE Polyamide-oligonucleotide derivatives, their preparation and use

JOURNAL Patent: US 6919441-A 38 19-JUL-2005;

Aventis Pharma Deutschland GmbH; Frankfurt;

DEX;

FEATURES Location/Qualifiers

source 1. .12

/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 13;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGCTC 10

Db 2 CATCATGCTC 11

RESULT 33

LOCUS AR699877

DEFINITION Sequence 48 from patent US 6919441. 12 bp DNA 1linear PAT 14-SEP-2005

ACCESSION AR699877

VERSION AR699877.1 GI:75205785

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE Unclassified.

1 (bases 1 to 12)

AUTHORS Uhlmann, E. and Breipohl, G.

TITLE Polyamide-oligonucleotide derivatives, their preparation and use  
JOURNAL Patent: US 6919441-A 48 19-JUL-2005;  
Aventis Pharma Deutschland GmbH; Frankfurt;  
DEX;

FEATURES  
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Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10  
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Db 2 CATCATGTC 11

RESULT 34  
AR699878/c AR699878 12 bp DNA linear PAT 14-SEP-2005

LOCUS AR699878 Sequence 49 from patent US 6919441.  
DEFINITION AR699878  
ACCESSION AR699878  
VERSION AR699878.1 GI:75205786

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Uhlmann,E. and Breipohl,G.  
TITLE Polyamide-oligonucleotide derivatives, their preparation and use  
JOURNAL Patent: US 6919441-A 49 19-JUL-2005;  
Aventis Pharma Deutschland GmbH; Frankfurt;  
DEX;

FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
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QY 1 CCTCATGTC 10  
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Db 11 CATCATGTC 2

RESULT 35  
AX283286 AX283286 12 bp DNA linear PAT 20-NOV-2001

LOCUS AX283286 Sequence 50 from Patent WO0179249.  
DEFINITION AX283286  
ACCESSION AX283286  
VERSION AX283286.1 GI:17044167

KEYWORDS  
SOURCE Synthetic construct  
ORGANISM Synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.  
TITLE Polyamide nucleic acid derivatives, agents and methods for  
JOURNAL Patent: WO 0179249-A 50 25-OCT-2001;  
Aventis Pharma Deutschland GmbH (DE)  
Location/Qualifiers

FEATURES  
source 1.12  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der kuenstlichen Sequenz:  
Oligonukleotide"

Query Match 42.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCATGTC 10  
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Db 2 CATCATGTC 11

RESULT 36  
AX711060 AX711060 12 bp RNA linear PAT 11-APR-2003

LOCUS AX711060/c Sequence 360 from Patent EP1288296.  
DEFINITION AX711060  
ACCESSION AX711060  
VERSION AX711060.1 GI:29787441

KEYWORDS  
SOURCE Herpes simplex virus unknown type  
ORGANISM Herpes simplex virus unknown type

REFERENCE 1  
AUTHORS Draper,K.G., Moswigen,J.A., Holecsek,J.J., Dudyecz,L.W.,  
Macejak,D.G. and Mamone,J.A.  
TITLE Method and reagent for inhibiting HBV viral replication  
JOURNAL Patent: EP 1288296-A 360 05-MAR-2003;  
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES  
source Location/Qualifiers  
1.12  
/organism="Herpes simplex virus unknown type"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:126283"

Query Match 42.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 12 TCATGTCAC 3

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